

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTCCCAAGGCCCTCCCTGTGTGAAGAATTCCATCACGAAGATCA
 ATGGCTGTTAAACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAAGAACTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTCATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAAGCCTGTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAAATATTAGGGGGTCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCCACTGTGGCCATGTGTGCGCCCAAGTGAAGAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCACCTCTTACTCAGTGGCAATGTACGGTGGATT
 AGTCTCTTTTACAGCATGTTCCCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAATAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCCAACAGAAA**GAATG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGCGAGATATGC
 ATTAATAAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCAATATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACACATTTCAATTCATGTTTGGAGTGATTTTAAATATGTT
 TTGGTGAATGTGAAAACATAAGTTTTGTGTCATGAGAATGTAAGTCTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAATTAGCAAACCTGTGTTGTCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCAATAGTGATTGGAGCTTTGGTAAAGGACAGAGAGAAG
 GAGTCACCTGCAGCTTTTGTGTTTTTAAATACTTAGAACCTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGAAACAAAGTGGTCATTGTTACATTCATTT
 GCTGAACCTTAACAAAACGTTCATCTGAAACAGGCACAGGTGATGCATTTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTCCAAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACATATCTCAAGAGAAAATATTCAAAGCATGAATATGTTGCTTTTCCAG
 AATACAACAGTATACTCATG

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 111111
 222222
 333333
 444444
 555555
 666666
 777777
 888888
 999999

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFWAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSIGSMFLPPTTVAGATLYSVAMYGGVLVFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCCCGCTCTCCGCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGCTCGTGAAGG
 GGTTCGGCAGCGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACTGTGGGTCTGAAGACATGTCGG
 ACATCGGAGACTGGTTTCAGGAGCATCCCGCGGATCACGCGCTATTGGTTTCGCCGCCACCGTC
 CGCGTGCCTTGGTCGGGAACTCGGCGCTCATCGCCCGGCTACCTCTTCCTCTGGCCCGGA
 AGCCTTCCTTTATCGCTTTTCAGATTTGGAGGCCAATCACTGCCACCTTTATTTCCCTGTGG
 GTCCAGGAAGTGGATTTCTTTATTTGGTCAATTTATATTTCTTATACAGTATTTATACGCGA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
 TGTTCAGTACTTTATCTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGA
 ACACGATTTAAGGCCTGCTATTTACCCTGGGTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTCCCTAATGTTCA
 GATACCAATGGACTTGGGAGGAAGAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTCGCCCATAGGAGAGGAGGATATCAGGATTTGGTGTGCCCGCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGAGCGGGAGACACAACCTGGGCGCAGGGCTTTCGACTTGGAGACC
 AGTGAAGGGGGCGGCTCGGGCAGCGCTCTCTCAAGCCACATTTCTCCAGTGTCTGGGTG
 CACTTAACAACCTGGCTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGCAAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTCCCAAAAGTTTACAGAT
 TCTCATTTCAAGTCTTACTGCTCTGGAAGAACAAATACCAAGTGTGCAAAATGTCAAACTGAC
 TACATTTTGGCTTCTCTCTCTCCCTTTCCTCTGAAATAATGGGTTTACGGGGTCTCT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAAGGACCTTATCTCTT
 TCTTGCACACATGCTCTCTCCCACTTTTCCCAACCCCAACATTTGCAACTAGAAAAAGTTG
 CCCATAAAATTCGCTCGCCCTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT
 ACAACAATCATATTACGCTTATTTTCCCTTTTGGTGGCAGAACTGTACCAATGAGGGGAG
 AAGACAGCCCGAGTGAAGCGCTTCTCAGCTTTTGGAAATGCTTCAGCTGACATCCGTTTGT
 AACGCTTTCACCTCTTCAGATATTTTATAAAAAAGTACCACCTGAGTTCATGAGGGGCA
 CAGATTTGTTATTAATGAGATACGAGGTTGCTGCTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAAGACTGTAGTGAAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCC
 TTTGCGTTTCATATGAGCCCTACTGGCTTGTGTAGCTGGAGTGTGGGTTGCTTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGTCCCTGGGCAATG
 ATTCCCAATTTCAATCTATTCTGGATATGTGTTCAATTGAGTAAAGGAGGAGAGACCCCTATA
 CGCTATTTAAATGTCACTTTTGGCTATCCCCCGTTTTTGGTTCATGTTTCAATTAATGTT
 GAGGAAGGCGAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAACACATCTA
 AGGGAATAAATCATGTTAAAGTTGAAATGGCTTTAGAATCATTTGGGTTTGGGTTGTGTTA
 TTTTGAGTCAATGAATGACAAGCTCTGTAATCAGACCAGCTTAAATACCCACACTTTTTT
 TCGTAGGTGGGCTTTTCCATACAGAGCTTGGCTCATAAACCAATAAAGTTTTTTGAAGGCCA
 TGGCTTTTTCACACGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTTAGGAGCAGT
 ATTGAGTGGCTGTACACATTTTGGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTCTT
 TTCAGGAACCATTTGCTCTTAACAGTATGACTATTTCTTCCCACTCTTAAACAGCTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTAATTTATGATAAAATAGTGGGAGAGCTGGAACCTTCACTTGTGTA
 TGTTTTGTTGTTCACTGTGGCCACAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
 CCAATTATGTGACGTACACTCATTTGACGGCTGGAGACTCATGTATGTATAAGAATA
 TTTCTGACAGTGTGAGTACCCGAGTCTCTGGTGTACCCCTTACCCAGTCACTGCTGCGGAG
 CAGTCAATTTTCTTAAAGCTTTACAAGTATTTAGAAGTTTCAAGTTCAGGGCAAAATGTTT
 ATGAAGTTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTTGATTTTGTCTGGAT
 ATGTTTCTGGAAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACA
 TGACAGTGGATTCCTTTTACCAATGGAATAAAAAAATCCTTATTTTGTATTAAGGACTTCC
 TTTTGTAAACTAATCCTTTTATTTGTTAAAAATGTAAATTAATAAGTCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

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FIGURE 5

GGGGCCGCGGCTTAGGGCCGCTACGTGTGTTGCCATAGCACCACATTTGCATTAACCTGGTTG
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCTAACCGGGGTCGGCGGTCTGGCCTAGGGATCTTCCCGTGTGCC
CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCTGCGAGGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCTTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTCT
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATGGAAAT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGC AAAAGCCCATACATCACAGGC
CATTTTGC AACCTGTGTTGGCAGCAGAA GATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATTCCAAAGGGGATGGTGAACATTTTGCACACCCACCCCTCAGAAGTTAAAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCTCCTCC
CACAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAAC
TTATCAGTACTTGAACAGAGAAGACTTCGGCAACGAGAACCATCTCAAGCAGAGAGAGA
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTTAACAGATACAAAATATGGAGCAGAAAG
GAAAACCCACTGGGAGGTTAGGGAATGACAGAGAAACGAGAAATGACAGCAGAGGAGAAAG
CAAACTACTTAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGTA
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTTGCTCTAAAAATAAATTATTTAGTC
CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEESKLTYTEIHQYKELVEKLLLEGYLKEIGINEDQFQEAQTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIIRIIQERNVGLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRRKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

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FIGURE 8

CGCTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTTACTG
 TCTCAGCTCTAGGATGTGCGTCTTCCACTAGAAAGCTCTTCTGAGGGAGGTAAATAAAAAAC
 AGTGGAAATGGAAAAACAGTGTCTAGTCATCTCTGTAATATGCTCCTTGTCAACATGTATAC
 ATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAACAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGTCTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAAATTTGAAATATGCTTCTGGAAGGAATTCCTGATTCATGAAGTGGTCCATTCTCGCCT
 TTCTTTATTTCTGGATAAATCTGATTGTCTTCTATGTCCTGTCTATCTTCAACAGGCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCAACACTTGGCAGGACGTGGATTTTCATCAGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCCTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTCTTATTTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACCCAGCTCACTGAAAGCATCTTCTATACA
 GAACAGCAAATCTTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAGAAGCTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTTGAACATGCATTCAGGGGCTTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGAATGGCCAGGTTACCACCTGCATATACACACAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCTGGAATTTTTCTTGGAGGCCCATAGTCTCTCTCTATA
 TTTTATTTATATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAAGCTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTCTAACTGGTACCACATAGTTTGCA
 GCTCTCTGAACCTTATTTTCACATTTTCAGTGTGTTGTAATATTTATCTTTTCAGTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGTCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAGGCTAAGAAATCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAGCTTCCAACAACTTGTAATATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAGT
 CTCTCCCTTTTAAACATTATAAAGCTAGGTTGTCTTGAATTTTGAGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTTCTAAACAGTTGGTTGAAGGACCTAATATC
 CTGGCCATACCATGCTTTGGGATGATGAGTCTGTGCTAAATATTTTGTGTAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATGGATTTTTGT
 AATAATCTTTGATGTTTTAAACATTTGGTTCCTAGTCAACATAGTTACCACTTGTATTTTA
 AGTCATTTAAACAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGTAT
 GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC
 CAGATTGTCAAGTGAAGCTGATGCCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAACACATGTTGACTTTTAACTGATGATGAATATTAATCACTTAAATAATAGAAAGACC
 AGTAATATAAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCATAGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAACAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACCTGAGCCCTGTATGTTTACAGACTACCACACTGTAAGATAGAGCTTTATGTGTG
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACATTATATAATTCATTGTGATATCCCAATAATATGACTGGCAGAATGG
 GTGGAATTTGTAATTAATAATATTATAAACCT

FIGURE 9

MEKQCCSHPVICLSLSMYTFLFGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFVCVLVSPCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFVVLVSYLQPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSHLYFFGILFENGLTLGLQRSNRDQIKNCGFFYGHSAFSAVALI
FVTAQGLSVAFILKFLDNMFKVLMAQVTTVITTVSVLVNDFRPSLEFFLEAPSVLLSIFI
YNASKPOVPEYAPROERIRDLSGNLWERSSGDGEELRLTKPKSDESDETDF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCGGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTTCGCCTATACCTACTGTAGCTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTC AACAAATGTATACATTCCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGTGAAGAGGCGCTAA
CTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

TGGTCTTTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTTGGGGGCGAGGAGCAT
 CCCGCTTACCAGGTCCCAAGCGCGTGGCCCGCGGGTCTAGGCCAAAGGAGAAGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCA
 GGTGAAGAAAGAACCAGAAAAAGAGAACAACAGTTGTCTGTTTGCACAAAGCTTTGTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCTTCCATCAGTCTAC
 CTATTGGC**ATG**TGGCTCAGGTGGGCCCCCTTTCTGTGCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCGCTCATTGGCCTACTTCCTC
 ATCTGGTTTCGTGCCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACATGGCACCCTTCCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCACTGTCTGTATCTATATAATCTG
 TGCTGTCTATCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCTGAGCCACGGCCCATACATCAAACTT
 ATTACTGGCTTCCTCTTCCACTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCCATCTGGCAGTGGTTCTTGACCGGTTTGGCAAGAAGCAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCTTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTCCACCAAGTTTGCTCTGGAGTGTG
 ACTGGGCATTTTACCTCAGTCTGGACTTTCGAGGTACACAGCCGCTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACTGAACATGCTCGTGACCATGGCTCCCATAGTTTCTCATCTG
 CTGGGCTGCTGCTCTTCAAAATGTACCCCATGATGAGGAGAGGCGGCGGCAGAAATAGAA
 GGCCCTGCAGGCACTGAGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCT**TAG**GGCCCCGCCAGCTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTGTGTGCTCACTGTGGGGCCGGCTGCTGTG
 TGGCTCTGCTCCTCCCTCTGCCTGCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGCTAGCCCGGAACACTAATGTAGAACCCTTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

MWLRWALS LPPSSCLWAEFGMP SQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFN SSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYITCAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLTSLAFMLVEGNFVLFCT
YTLGRNEFQNL LLAIMLSATLTIP IQWQFLTRFGKKTAVYVGISSAVFFLILVALMESNLI
ITYAVLVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVF TFKFASGVSLG
ISTLSLD FAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILLGLLLFKMYPIDEERRQNKAL
QALRDEASSGCSCTDSTELASIL

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

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FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAGCAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCATTTGTGGCAAACCTCCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTAGCATGCTGACTTGCTCATCAGTTTTCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAAACAATGAACGAACACGGCTACTTCCAGAGATATTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTAACAAACCTATGCCTATACCTTTTATCTCAGAAAAATAAGTCAAAGACTATG

MWWFQQGLSFLPSALVIWTSAAFIIFSITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLICATIYVRKQVHALSPEENVIIKLNKAGLVGLISCLGLSVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYMQPKIHGKQVFWIRLLLVICVGSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAEWSMSSFSFPGFFLTYYRDFQSLRVEANLHGLTLYD
TAPCPINNERTRLLSDRI

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCGTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAATCAGCGGTCTAATTAAATCTCTGGTTGTTGAAGCAGT
TACCAAGAACTCTCAACCCCTTCCCACAAAGACTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCTCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAGAGGCCCTAGGTTTCCCTCCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTTCATATTTTCATACATCTAGTCGAGTAACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGAC**CATG**CGCCCGCTTCTCGGCCCTCCTTCTGGTCTTCGCGGGCTGCAC
 CTTGCGCTTGTA^{CT}TTGCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCC^{CT}CCGACCTGGCAGAGCTGCGGGAGCTCCTCTGAG
 GTCTTCTGAGAGTACC^{CGA}AAGGAGCACCAGGCC^{TAC}GTGTTCTGCTCCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTTGCCATCCCCGCGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTGTTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAA^{ACT}GGTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAA^{TT}CCTGGAACCTCATTA^{AAAA}AATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACA**TGA**TCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCCTCTAAAGCCCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTT^{CAG}AAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCGGGGCGCGTGGCTCAGCCTGTAATCCCAGCAC^{TT}TGGGAGGCCGAGGCCGGTGATT
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATA^{AAAA}AAT
 ACA^{AAAA}ATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCAC^T
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
 KEHQAYVFLLF CGAYLYKQGFALPGSSFLNLVLAGALFGFWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPDKVALLQRKVEENRNSLFFLLFLRLFPMPNWFNLNSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKFKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

CCGAGGCGGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTCTGCTGCCAACGAGATCAGCA
TTTATGACAAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAGAAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
GGAGTCTCACACCTGGCGCTCACTCATTCATCACATTAGGCTGATGTCTTGCCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGAGTCTCTCTGCATGGGGGTGATCAAGACAGACCCCTTTC
CAGACTTTGACCCCTGGTGGACAACAGCATGTGTAGCAGAATGAGTCAGAGCCCATTTCTCGCC
AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCCCAA
GTGGTGGCGCTGCTTCTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCTACTCACTGCCATTTCCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
ACCAACCCACTGGAAGGCTACGTTATAGCCAGAGGGGTCAGCCTTTTGGTCATCTCGCAT
AGAACCGCTTTCTCAGAACTGTAGGAAATAGAGCTGCACAGGAACAGCTTCAGAGCCGA
AAACCGAGTTGAAAGGGGAAAAATAAAACAAAAACGATGAACATGCAAAAAA

MDLAANEISIDKLSETVDLVRQTHGQCGMSEKATEKFI RQLLEKNEFORPPFPQYPLLI VVY
KVLA TLGLILLTAYFVIQPFSP LAPEPVLGSAHTWRS LIHHTRLMSLP IAKKYMSENKG VPL
HGGDEDRPFDFDFPWWTNDCEQNESEPI PANCTGCAQKHLKVM LLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEPGVSEGFFAKWWRCSFWRWFPPYPWRRLNRSQMLRELFFV
FTHLPFPK DASLNKCSFLHPEGVSGKMKHMDPLFIISGEAMLQ LIPFPQCRRHCSVAMP
IEPGDIIYDSTTHWKVYIARGVQLPVICDTAFSEL

CCACGGTGTCGGTTCTTCGCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAAATAGGAAAATAACTTGGGATTTATATT
GGAAGACATGGATCTTGTCTGCCAACGAGATCAGCATTATGACAAACTTTT CAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCTAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCCGACGATATCCTCTCCTTATAGT
TGTGTAATAAGTTCTCGCAACCTTGGGATTATCTTGCTCAGTGCCTACTTTGTGATTCAAC
CTTTTCAGCCCTTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGTGTCTCCGGCTGGTG
 CCAGTGGTGGCCAGCTGCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGAGTCTGCC
 CTCCTCGCCACCCCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGGCA
 ACCCGAATGGCCGCACTTCATCGACAAACAGGTACAGCCAACCATGTCCAGTTTCGAATT
 GACACGATGCTTAAGAGCCACGACCTTATGTCAGGTTTCTGGAATGCTGCTATGACATGCT
 TATGAGCAGTGGCCAGCGGCCAGTGGGAGCGCCCGAGCTCGTGGGGCTTCCAGGAGT
 TGCTGCTGGAACCTGCGCAGAGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGTG
 AAGCAGGCAACGCGACACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCATGTGGGGCTTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGTGCCAACCATCACTTCGACCCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTTCCCTGACACCCACGAGGAGGC
 GCACTGCTCTGGCAGTACCCAAAGAGGCCAAAGTGAGCACCCCAAGTTCGCGAGGTGCTG
 AGGACAGCTCGCGGAGGACGAGCTGCTGAGCTGGAGACCCGATGGAGGCAGCAGAAGCTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGGCGCCAGCTGGTGACGGTAGTGGCCCT
 GGTCCCAGGGCTGCTGGAGGCTACCACACAGAATGTACTTCTACGATGGCAGCAGTGAAG
 GCTGGAACCCGAGGAGGCGATCGGCTATGATTTCCGGCGCCCATGGCCAGCTGCGTGAG
 GTCCACCTGGCGCGTTTCAACCTGGCGCGTTGACAGCTTGAGCTCTTCTTTATCGTACAGGC
 CAACTACTTCTCACTTCCCATGCAAGGTGGGCACGACCCAGTCTCATCTCTATGACGAGA
 CTCGAGGTCGCCAGCTGGCCCCATCCCAACCCATACCCAGGTCAGGCAACAGGTTGATCTCG
 TGCTCTGTCGCGCTACGGCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCGAGAGAT
 GCTCGCTGCTCAGGCTTACCAGAAATGGGTACAGCTGAGATATCCAATCTCGAGTACT
 TGATGACTCAACACATTTCGGGGGCGGACCTCAATGACCTGTCTCAGTACCTGTGTGTT
 CCCTGGGTCTTCAGGACTACGTGTCCCCAACCTGGAGCTCAGCAACCCAGCGCTCTTCGG
 GGACTGCTTAAGCCCATGGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAAGAT
 ATGAAGCTTTGAGGACCCAGCAGGAGACCATTGACAAGTTCCACTATGGCAACCCACTCC
 AGGCAGCAGGGCTGATGCACTACCTCATCCGCTGGAGCCCTCACTCCCTGCACGCTCCA
 GCTCCAAAGTGGCCGCTTGTACTGCTCCGACCGGAGTTTCCACTCGGTGGCGGAGCGCTGGC
 AGGCAGCTGTGGTGCTATCCCGCTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCCGC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACTATGA
 GGGGCTCTAGACCTGGACATGTGACAGATGAGCGGGAACGGGAAGGCTCTGGAGGGCACTTA
 TCAGCAACTTTGGGCAGACTCCCTGTGAGTGTGTAAGGAGCCACATCCAACCTCGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCCTTGCAGCCTGGACACTAACTCAGCTAGCATCTTCCAGCA
 CCTGGACGAATCAAGGCATTCTTCGAGAGGTGACTGTGAGTGCCAGTGGGCTGTGGGCA
 CCCACAGCTGGTGGCTTATGACCCGCAACATAAGCAACTACTTCAGCTTCAGCAAGACCCG
 ACCATGGGACGCCACAAGACGCAAGCAGCTGCTGAGTGGCCGCTGGAGGTCAGGAGTGGTGT
 GAGTGGACAAGCAGCTGGCAGTGGCCCGGATGGAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGAGCTGGCGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCGCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCTTGCATGGACACCTGTGGCATCTACCTCATCTCAGGCTTCCCG
 GGACACCAGCTGCTAGTGTGGCGGCTCCTGCATAGGCTGGTGTGCTGAGTAGGCTGGCAG
 CAAAGCTGTGCAAGTTCCTGTATGGGCTAGGGGCTGCAGTGAGCTGTGTGGCCATCAGCAGT
 GAATGTGACATGGCTGTGTCTGGATCTGAGGATGGAACGTGTGATCATACAGCTATGCGCG
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTTCCACC
 TGGCTATGGGTCCGAAGGCCAGATTTGGGTACAGAGCTCAGCTGGGAGACGCTGCTGGGGCC
 CAGGTCACTACTCTCTTGCACCTGTATTGATCAATGGGAAGTTGCGGGCTTCACTGCGCCCT
 GGCAGAGCAGCTCAGCCCTGACGGTGCAGAGGACTTGTGTGCTGCTGGCACCAGCCGAGT
 GCGCCCTGCACATCTCCAACTAAACACACTGCTCCCGCGCCGCTCTGCTTGCCTATGGAAG
 GTGGCCATCCGAGCGTGGCGGTGACCAAGGAGCGCAGCCAGTGTGGTGGGCTGTGAGGA
 TGGAAGCTCATCGCTGGTGTGCGGGGCGAGCCCTCTGAGGTGCGCAGCAGCCAGTTCCGCG
 GGAAGCTGTGGCGGTGCTGCTGCGCGCATCTCCAGGTGCTCTGGGAGACAGCGAATACAAC
 CCTACTGAGGCGCGCTGAACCTGCGCAGTCCGGCTGCTCGGGCCCCCGCCCGCAGGCGGTG
 GCCGGGAGGCCCGCCGGAAGTCCGGCGGAACACCCGGGTGGCAGCAGCCAGGCGGTGA
 GCGGGGCCACCTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGAAGTCCCGCCCTCGCGGCTGAGGGGCGCCCTGAGGGCGACTGCGGCTCT

FIGURE 23

MSQFEMDTYAKSHDLSMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMAALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAEELETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPHPTQV
 RNQVYSWLLRLRPSPQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSPKIGVVPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEFFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKELIP
 EFFEYFPDFLENQNGFDLGLQLTNEKVGDVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGII SNFGQTPCQLLKEP
 HPTRLSEAAEEAHRRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGMSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCIALDTCGIYLLISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGGIVVQSSA
 WERPGAQVITYSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDEGKLIVVVGQPSSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTCAATCTGCAATCTATGGGGTCTTGGGGCTCTTC
 TGGACCCCTTAAGTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGAGCAAAAGTCACAGA
 CCTGCTGCTGTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTACGCGT
 TTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGA
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTtagGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACATTTGAGAGGCTG
 AGGCGGGCGGATCACTGAGTCAGGAGTTCGAGACCAGCCTGGCCACATGGTGAACCTCC
 GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGCACTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAGATATTTTGTAACTC

RTGRTRGGCEKVPINTSCNPTAHLVNSSCPLGMLCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWLVALGQCVLGAFASFYWFHKKPQDIPTEPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLGRGVNPARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAK
NAFMLLMRNIVRVVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPLGKDFKSPHLNYY
WLPIMTSLILGAYIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMKSLLKILGKKN
EAPPDNNKKKY

FIGURE 26

GAGTCTTGACGCCGCCGGGCTCTTGTTACCTCAGCGCAGCGCCAGGCGTCCGCCGCCCGT
GGCTATGTTCGTGTCCGATTTCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT
CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAAGCTTGAAACTGC
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTTATTCTCATAACTGTGGAGCTAATGTAG
ACCTATTGGATATTCTTCAACCTGATGAAGACATATATTCTTTGTGTGTGACTCCCATAGG
CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
CAGGAAATGACAGTGATGGGTCCAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGAGAAGAGACATCCT
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGGCATGTTGATGTTTGAGCTGG
CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACAACACTCTCCGTGGACTGCA
CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTACACGACTGGTCCCTCCATGAC
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
GCGGCTCCAGGAGTTCCTTGACAGATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAAGTTCC
AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
TTTGGGATGAAGGACATGCGCGTGACACTTTCAGCATTATTTGGGTTCAAGCACAAGTT
TCTGGCCAGCGACGTGGTCTTGGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
TACCATGGCTGGAAGCTCGCAAAGAAGCAGCTGCGAGCCACCCAGCAGACATTGCCAGCTGC
CTTTGCACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
AGTCTTTGTGTGTTGACAAAAGACCGGCGCTGCAAAGTGTGCCCCCTGGTGTGGCTGCC
CCCCCTGAGCATGGAGCATGGCAGTGACCGTGGTGGGCATCCCCCAGAGACCAGCAGCTC
GGACAGGAAGAACTTTTTGGGAGGGCGTTTGAAGGCAGCGGAAGCACCAGCTCCCGGA
TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
CTGGACGCACCTATTTCCCTCCTGTCTCTAGGAATTTGATCTTCCAGAATGACCTTCTTATT
TATGTAAGTGGCTTTCATTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
TTTTATTAAATAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAFL
LEHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAVEDIFRDEEEDDEHSGNDSGSEPEKRTRLEEEIIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFYCSLMEGT PDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

09990441.11501

GTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCGTGCGTATGNTCGTGTCCGATTTCGCA
AAGAGTTCACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCAATTTTTCTAGTGAAC
 CAGGAAGGGGACGATACCAGAAAAACCCCTCAACCCAAAGGAATAGACTACAGCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTTACAGCTTTTAACAAT
 GACTAAAGTAGCCTCCGGTCAAC**ATGG**TGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCCTGATGTGTGAGATCCGATAGTGGAGCTCACCTTTGACAGAGTCTGGGC
 CAGCGGCTGCCAAGCGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG
 CCTCTTCTCCGGCCGCCACGCCCTGCTGAGATCAGACCTTACATTAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCCTGCCAGGGTACATGGGCAGGAGGG
 TCCCCAAGGGGAGCTTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG
 GCGCCCGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAG
 GCGGAGGACTTCCAGACGCTGCTCTTGAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGGCACGGCCAGTTTGTCTGCTCCCTTGCCTGGCATCTACTTCTCAGCCTCAATGTGC
 ACAGCTGGAATTACAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCTC
 CTGTACGCGCAGCCAGCGAGCGACGATCATGACAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGGAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTCAAGCGCCACCTCATCAAGGCCAGGACGAC**TA**AGGG
 CCTCTGGGCCACCCCTCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGGAAGCGAAGGCCAGGAGGTCCCGGGGACCTGGCATTTTGGGGAG
 CCGTGCTTATCTTTGGCTGGCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCT
 TGGACTTTATTTAAGAGCTTGCTAACCTAAATATTCTAGAATTTCCAGCCTCGTAGGCC
 AGCACTTCTCAAACTTGGAAATGCATGCGAATCACCCCGGGTTCGTGTTAAATGCAGATTCT
 TACTCAGCAGCTCTGAGTGGGTCCAGGATCTGTGTTTCTCATATGTTCTCTGGGTGATGCTG
 ATGGGTCAGTCTATGAACCACTGGAGCAACAGGTTCCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCTCCCCACATCTAGAATTCTCCAACATTTTTTTTTCT
 TAGACAGAGTCTTGTCTGTTGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTCACTGC
 AAGCCTCTGCTCCCGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTCC
 AGGCGCTGCTTACCATGCTTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCCACATA
 TTGGCCAGGCTGTTCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCCTCGAAAT
 GCTGGGATACAGGTGTGAGCCACCGTGCCCTGGCCCAATTTCAACATTTCTTAAATCTCTCAT
 CCTCTCAGGGCTCCCGTGTATGTTTCTTTACCCCTTCCCGCTTCTCTTGTCTCAGGCC
 TGCACCCTCAGCCACCGTTTCAATTTATCATTATTAACACTGAGCACTCAGTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTGCAGACACAGGCCCTGCCCTGCCCTCAGTGCAGCC
 GTCCAGCCCAAGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGTCTGGGG
 GCGTGTGTTCTGGGTGTTCAAGTGCTGCTGGTCTCCATTACCCACTGCTCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGCGAGTATCTCTTCCCGTTCCTCATCCACTGCCGAC
 TGCTCATCGTTACAGCAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCAGGAGTGTGGGGGCTATTGGGGGGTGAAGTGGCCCCGAAGAAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTCTGCAGAGAAGACTGCCCTCCTCAGTGGATCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAAGTCACT
 GAACCTCCGTTTCCCAAGGGCTCCAGCTGCCCTCAGACACTGATGCTGTCCCCAGGCTGCT
 CTCTGCCCTCATGCCCTCTCACCGGCCAGTCCCCGACTCTCAGGCTTTATCAAGGT
 CTAAGCCCGGGTGGCGAGCTCTCGTCTCAGAGCCCTCCCGCTGGTGGTCTGCTGCTTTAC
 AAACACCTGCAGGAGAAGGGGCCAGGAAGCCCGAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGAGGGGACCTCAGGCCTTCGGTTTCTTCTTCCAGGGTGGGGTGGCTGGT
 GTTCCCTAGCTTCCAAACCCAGGTGGCCTGCCCTCTCCCCAGGGAGGGCGGCCCTCCGC
 CCATTGGTCTCATCAGACTCTGGGGCTGAGGTGCCCGGGGGTGTATCTCTGTGGTCTCAC
 AGCCGAGGGGAGCGGTGCTTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCACGA
 AGACTGTGCTATAAACACCTGCTTGCATCTGCCCTGCTGACCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGAAATGCTGCTCCTCTTGGAAAAAAGAAAAA

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FIGURE 30

MVTAALGPFVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCGCAGGAAAGACTG
 AGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCCGCGCTCCCGGACAGAAAGATG
 CTCAGGGTCCCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCACTCGGCTGCCAGTGCAGGCAGCCACAGACAGTCTTCTGCCTGCCCGCCAGGGG
 ACCACGGTGCCTCGAGACGTGCCACCCGACACGGTGGGGCTGTACCTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTAC
 AGAACCAGATGCCAGCTGCCAGCGGGTCTTCCAGCCACTCGCAACCTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATACCAATGAGACCTTCCGTGGCTGCGCGCTC
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCTCTGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCGTGGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT
 CCTGGCACTGCCAACCTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTACGCCCTTTCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTCGGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGCTCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTTAAGCTCGAGGCTGCTGCTGGGACCTCTCGGGCTCTTCCCGCCGCTGCCG
 CTGCTGGCAGTGCCTCGCAACCTTCAACTGCTGTGCCCTGAGCTGGTTGGCCCTCG
 GGTGCGCGAGAGCCACGTACACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACAG
 ACCACAGCCACAGTGCCTCCACAGGCGCTGGTGGGGAGCCACAGCCTTGTCTTCTAC
 CTTGGCTCCTACTGGCTTAGCCCCACAGCGCGGGCACTGAGGCCCCAGCCCGCTCCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCCAGCCCCAGGACTGCCACCCTGCCCTGCCCT
 AATGGGGGCACATGCCACCTGGGGACACGGCACCTGGCGTGTGTGCCCGCAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCGCCACCTCCCTGCGC
 GTGGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCTGCTCGCTCGCTG
 AGTACACGGTCAACAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCCTTTGGGG
 CCGGGCGGGTGCCTGGAGGGCGAGGAGGCTGCGGGGAGGCCCATACACCCAGCCGCTCCA
 CTCCAACACGCCCCAGTACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTATTGGCCCG
 CCTTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACAGCTACTGTGTGCGGCG
 GGGCGGGCATGGCAGCAGCGGCTCAGGACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC
 GGAATGGAGGAGTGAAGTCCCTTGGAGCCAGGCCGGAACAGAGGGCGCTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGCTGGCCTC
 CAGTACCCCTCCACGCAAGCCCTACATTAAGCCAGAGAGAGACAGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACACAGTAAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGGCTGTTCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCCTAGGAGACGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAGCGG
 GCGCTGCCATGTGTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCACTCCAGCGCGGA
 CTTTGGGGGCTGAAGGAAGCTCCCGAAGAGCAGAGGAGAGCGGGTAGGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCAAGGAACAAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATTCTG
 GGAAGATGTTTTTAAACTCAGAGCAAGGACTTTGGTTTTTGAAGACAACAGATGATATG
 AAGGCCTTTTGTAAGAAAAATAAAAGATGAAGTGTGAA

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FIGURE 32

MCSRVPLLLLPLLLLLLALGPGVGQCPGSGCQCSQPQTVFCTARQGTTVPRDVPDPDVLGYLVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLRLYLGNRIRHIQPGAFDTRLRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNHLDDLVDSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCLPSWFG
FWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPTVPVGPVQPQDCPSTCLNGGTCHLGRHHLACLCE
GFTGLYCESQMGQGRSPSTPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRL
TYRNSLGPDKRLVTRLRLPASLAEYVTVQLRPNTATVSCVMLPGVGRVPEAAEAGEAHTPPA
VHNSHAPDVTKAREGNLPLLIAPALAAVLALAAVGAACVVRGRGMAEEAQDKGVPGAG
PLELEGVKVPLEPGPKATEGGEGALPSGSBCEVPLMGFPGLGLOSPLHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATTCATCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAAAATCAATGAGACTCATCAG
 AAACATTTCACATATTTTGTAGTATTTGTTATGACAGCAGAGGGTGATGCTCCAGAGTGGCCAG
 AAGAAAGGGAAGCTGATGACCAACTGCTCCACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCCAGGCCACACGACATCGGATTTATCCCTATAACCTCCTTTCACTCCAGAGTTTCAGA
 TTTTCATTTCTGTCCCAACTGAGAGTTTGTATTCATGCCCATAACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTAAATACAGACTG
 AAGAGTGTAACTTTGGTATTTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAAATTGCTCATCTGCATCTAAATACTGTC
 TTTCTTAGGATTCAGAACTTTCTCTCATTATGAAGAAAGGTAGCCTGCCCATCTTAAACACAAC
 AAAACTGCACATTGTTTTACCAATGGACAAAAATTTCTGGGTTCTTTTGGCGTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAATTTGTAGTTATGAA
 ATGCAACGAAATCTTAGTTTGA AAAATGCTAAGACATCGGTTCTATTTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
 TCAAAATCTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGGATATAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATCTAAATG
 CACAAATGGCCACATGCTTTTCCGAAATATCCCTACGAAATTTCAATATTTAAATTTTGGC
 AATAAATCTTTAACACAGCAGGTGTTTAAAGAACTATCCAAGTCCCTCACTTGAAAACCTCT
 CATTTTGAATGGCAATAAATCGAGACACTTTCTTTAGTAAGTTGCTGTTGCTACACACACAC
 CCTTGGGAACCTGTGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA
 TGCCCAAGAACTGTGGTCAATATGAATCTGTCAACAATAAATGCTGATCTGTCTTCAG
 GTGCTTGCCCAAAAGTATTCAAATCTTGACCTAAATATAACCAAAATCAAACTGTACCTTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAACAATAATTTGCAATTTAAATTTTCAACTGAT
 CTCCTCGATCGAGTCATTTAGTAGACTTTAGTTCTGGAACATTGAAATGAACTTCATTTCT
 CAGCCCATCTGTGGATTTTGGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATGCGGGAAGAA
 ATCCATTCGGGTGTACCTGTGAATTA AAAAATTTTCATTAGCTTGAAACATATTTCAGAGGTC
 ATGATGTTTGGATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACCTAG
 GTTAAAGACGCTTCTATCTCCACGAATTTATCTTGAACACAGCTGCTGTTGATTTGCACCATTT
 TGGTTATTATGCTAGTATCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACCAACCCA
 AGAACAACTCAAGAGAAATGTCGGATTCACGCAATTTATTTTCATACAGATGAACATGATTCCT
 TGTGGGTGGAAGAAATGAATGTATCCCAATCTAGAGAAGGAAGATGTTTCTATCTTGATTTGC
 CTTTATGAAAGCTACTTTGACCTTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCAATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGCCACCAACATCTCTCCATGAAAATTTCTGATCATATAAATCTTTATC
 TTTACTGGAACCCATTCCATTTCTATTGCAATTTCCCAAGGTATCATAACTGAAAGCTCTCTCT
 GGA AAAAAGGCATACTTTGGAATGGCCCAAGGATAGGCGTAAGTTGGGCTTTTCTGGGCA
 ACCTTCGAGCTGCTATTATGTTAATGTATTAGCCACAGAGAAATGTATGAACTGCAGACAT
 TTCACAGAGTTAAATGAAGAGCTCGAGGTTCTACAATCTCTCTGATGAGAACAGAGTTGTCT
 ATAAATCCCAAGCTCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTTGATA
 CAACCTTTACTTTTGGCCACCAACATCTCTCCATGAAAATTTCTGATCATATAAATCTTTATC
 TCGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACACCTTACAAGTTTATAAGG
 GCTATTGTGAAAAGAGTGTTCATCCAGGATTTGTTTATGAAATGAGTGGCCAGAGGTGC
 AGTGGCTCAGCTCTGTAATCCCAAGCACTATGGGAGGCCAAGGTGGGTGAGCCACGAGGTAA
 GAGATGAGGACCATCTGGCCCAACATGGTGAACCCCTGTCTACTATAAAATGCAAAATTTA
 GCTTGGGCGTGATGGTGCAGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGGATTCG
 CTTGAACCCGGGAGGTGGCAGTTGCAAGTGAAGTGAAGTGCAGGCCATGCACTGCAGCCTGGT
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAATGAAAAACATCC
 TCAATGGCCACAAAATAAGGTCTAATTCATAAATTTATAGTACATTAATGTAAATATAATTA
 CATGCCACTAAAAAGAAATAGGTAGCTGTATATTTCTGGTATGAAAAAACAATATAATAT
 GTTATAAACTATTAGTTGGTGGCAAAACATAATGTGGTTTTTGGCAATGAAATGGCATTGAA
 ATAAAAAGTGAAGAAATCTATACCAGATGTAGTAACAGTGGTTTTGGGCTGGGAGGTTTGA
 TTACAGGAGCAATTTGATTTCTATGTTGTGTATTTCTATAATGTTTGAATTTGTTAGAAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTTEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFAANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENCNWPETVVNMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMLRELNI AFNFLTDLPGCSHFSLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETTYSEVMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVFCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEFYFAHNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPDKRRKCGLEFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

GGGGCTTCTTCGGGCTCTTGCTTTGGAAACACTGCTCCACGAAGACCGGCTCTCGGAGGGGTGCGCGGGGAAGG
 CAGGAGGAAGAAGAGGCGGGGCGGGCCGCCCTCCGCGGCGCCCGCGGCTCTGCGCGCCTCTGCTCGCCCGGAGG
 CGAGCCAGGCGCAGCGCGCGGGCGGGTCCACAGCGCAGCGACCGCGCTCTCCGCGCCCCAGTGCAGCGCGCTCT
 CTGCTGTGCCCTCTGCGCCCTTGCCCGGGCGACGTTCTGCGCGCGGCGCGCCGCGCGCCCGGTGACCGCTGA
 CCTGCGCTCTGGGCGGGGCGGAGCAGCGATGTCTCCCCTCGGGGACCTGACCCAGCGCTGGTGCTCT
 CTGGCAGTGAACCTCGCGGGGTGGAGCGCCAGGCGCAGCCCTCGAGGACCTGATTATTACGGCGAGGAT
 CTGGAGCGGGAGGAGCTATACGCGCGCGGAGCCGAGCTCTGAGACCTTCTCTCGCGCGCTGCGCGGGG
 CGGGGAGGAGTGGGAGCGGGCGCCCGAGGAGCGCAGGCGCCGAGGAGGGCCAAAGCCAAAGACTCCC
 AAGAGGGAGAGTCCGCTCGGAGCGGCTCCACAGCTGTAACACAGCAACCAACAAATTTATGACACCAAG
 CTCTGAGAAGCTGCCACGATGATCACAGTGTCTGCTGTGGCCGTGAAGATGTACAGAGAGTGTGCCACT
 TTGGTCTGGAAACTTAAAAATCAAGACTTCCAGCTTCATGCTCCACGTTGAAGCGGATTTGSCCTGGGGCA
 CTGAGGAGGAGCTACCACTCAGCGGGGACTTAATGAAATGATTTTATGACGCGCTGTGGTGGCGGGG
 AATATGACTCCAGAGCTGATTGTAAGTGGGATCTCGGCGCTGACGAGATTCTAGTGGTCTCATCACTACAGGA
 GGAATCTCCCTCTGCTGAGTACCTGGGTGATCTCCTAATGAGCTGTGTGAGCAATGACGCGCACCGTGGGT
 ACTGTTTAAGATGTGATGTGGAGACATGATTTTGGAGAAAACAGTGAAGAGAGATCCCTGTTCTCAATGAT
 ACCCTGCTCCCATGTGGTGGCCGCTACATCCGCTATAACCTCAGTCTGTTTGTATATGGAGAGATCTGCAAT
 GATGAGAGATCTGGGTGGCTGCCACTGCGAGTCTTAATTAATTTATCACCGCGGAACGAGATGACCAACT
 GATTCACTGGATTTTAAGCACCACCAATTAAAGAAATGCCGCACTGTGAAGATTTGTAATGAATTTGTCC
 CAATATCACAGAAATTTACAAACTTGGAAAAGAACCCAGGCGCTGAGTCTGTATGCTGTGGAGATCTGAGT
 ACCCTGGGAGCAATGAAGTCTGCTGAGCCAGATTTCATCACTACCGGGGGGCGCCGGAACATGAGTGTCTGGG
 CGGGAGCTGCTGCTGCTGTGTGCAATCTGTGTGTGAGGAGTCTTGCCCGGAATTTGCCCGGAATCGCGCAT
 GTGTGAGGAGAGCCGCGATTCACTGCTCTCCCTCCCTCACCGCGGATGGCTACAGAGAAGCGCTACGAAGGGGCT
 CGGAGCTGGAGGGTGTGCTCCTGGGACCTGAGACGACTGAAGATGACATCAACAACTTTCTGATTTT
 AACACGCTGCTCTGGGAGCAGAGATGCAGAGAATGTCGCCAGAGAGTTCCTCAATCACTATTTGSAATCCC
 TGAGTGGTTTGTGTGGAAATGCGACAGGTGCTGCCGAGACAGGAAGCTCATGAGCTGATGGTGGAAAAATC
 TTTTGTGCTGGGGCGAACTCTCGAGGGCGGGAGCTGTGTGGGTGATTCCTACAGACTGTTGGGTGCTCCCC
 TGAAGAGAGGAGAAACACCCCCAGCCCGATGACAGCTGTGCTGGTGGCTACTCTCTGTGCTCTCAC
 ACACGCGCTCATGACAGACGCGCGGAGGAGGGTGTGCCACAGGGAGCTTCAGAAGAGGAGGGCACTGCA
 ATGGGCGCTCTGCCACACCTGCTGGAAGTCTGAACGATTTCAGTACTCTCAGAAAGACTGCTTCGAACT
 TCGATCTAGCTGGGCTGTGATAAATCCCACTGAGACGACGCTGCCGAGGAGTGGGAGATACCGGGAAT
 TCTGTGCTGTGTTCTAGGACGAGTTTCACTGTGCACTTAAAGCTTTGTGTAGAGATTCACTGGAATAAGCAATC
 CAAACGCCATATTCTCGTGAAGGCATTAACCATGACTCGAACACGCCAAGATGGGAATTACGTGGCTCT
 TGAACCGTGGAGATGTGTTGTACAGAAAGCGCAAGTTTCTAGCTACCCACGAAGACTGTGTTGTGG
 CTATGACATGGGGGCGCAAGGTGTGACTTCACACTTACGACAAACCAACATGGCGGAGATCCGAGAGATCATGG
 AGAAGTTTGAAGACGACGCGCTCAGCCTGCCACGAGCGGCTGAAGCTCGGGGGCGAAGAGACAGCAGCG
 GGTGACCTCTCGGGCGCTTGAGACTGCTCTGGGACGATGCAAAATTAACCAACTCTGGTAGTGTGCTCATG
 TGGACTCATCACTGTGTTTCTCTGTGTAATCAAGAGTGTCCGGAAGAGGGTGCATTGTGAGGCAAGCTC
 CAAAGAGGAGGCTGAGGCTGAGGCTGAGGCTGTTTCTTTCTTTGTTTCCATTTATCCAAATTAATCTGGACAGCA
 CGAGAGAAAGCTGATGGAGTGAAGAGAACTCAGACAGCCAACTCGGAAATCAGAGAGAGAAGGAGAGAGG
 GAGCTGTGCGCTTCAGAGCTCTGCGTGCAATGAAGAAAGATTGTGTTGTTCTCCCTGTTTGTGCGACAGAGG
 GTTCCACGTGTGATTTGCAATTTCGACAGCTAAATTTGAGCAATTTCCCGAGTGGGCTGCCAAATGTTTACA
 TTTGAGTGCTGCCAGCGCTCTAAGAGATCAACCTCTCTGGCGCTGGGACCTGTCAAGCTGTCTCAAAATAA
 TTTGCTGTGTTCTTTGACATAGCTCATTCGCAAGTGACATCAGTGAAGCTTGTGAATCTGTTTAGTCTCT
 TTTTCAACAAAGGGTGTTTCAACAAAGGAGAGAGAGCGCTAGATCATCTCAGGATTTGTGGGCGCAGCA
 TGGAGCTCTTGCTGCAAAATCTGGGTGCTATAAACACCCCAAGTCCCTGCTGATTCAGTGAAGCTGGAGGT
 CCCCAGTAGGAGAGGACGAGGTGCGACGCTCTTGAGGCGCAAGAAATTTAGCTGGATCTCCTCTTTTAC
 TCGTAGGACTGGAAGAGGCGCAAGTGGGTGGCGCTGAAGCGCTCTCTGCTGAGGATTGCGCCTTTGTG
 GAATTTAGTGTCTATGGGCTTTGGCTCATATCAGCTGGGAGTATTTTTGATGTAGATGCGAGTCTTCCA
 GATTAGGCTAAATGTAATGAARAACTCTTAGATTATCTGTGGAGATCATGATTTGGGAGAAATTTGTAATTA
 CTGTCGACAAAAAATGGTCTTCACTAATTTTGTGTAATGTGCTGCTCACTGACCTGGGAAAAATGAAAAA
 AATAAGCAAAATGGTATGACCTTTAAAAAATAAATAAAAAATAAATAAATAAATAAATAAATAAATAAATAA

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYQGQEIWSREPPYARPEFELETFSPPLP
AGPGEEWERRPQEP RP PKRATKPKKAPKREKSAEPPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGLRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWTVKNGSGDMI F
EGNSEKEI PVLNELPVPMMVARI RINPQSWFDNGSICMRMELGCLPLDPNNYYHRRNEMTT
TDDLDFKHNNYKEMRQLMKVVNMECPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARI VHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGI D INNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAMWEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNARESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKMRMGVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLRCGRKRRORG

FIGURE 37

CTAAGAGGACAAGATGAGGCCGCCGCTCTCATTTCTCCTAGCCCTTCTGTTCTTCTCTGGCCAAAGCTGCAGGGG
 ATTTGGGGGATGTTGGGAGCTCCAATTCCAGCCCCGGCTTCAGCTCTTTCCAGGTTGTGACTCCAGCTCCAGG
 TTCAGCTCCAGCTCCAGGTCCGGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCCCAATTTGT
 TTCCAATTTCAACCGGCTCCGTGGATTGAACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTC
 CCGTGGACAGAGTGGAAAGCTTGAATTCACAGCTCATGTTCTTTCTCAAGAGTTTGGAAAGAGCTTTCTTAA
 GTGAGGGGAATATGTCCAATTAATTAGTGTGTATGAAAGAAACTGTTAAACCTTAAGTCTCCGAATTGACATCAT
 GGAGAAGGATACCAATTTCTTACACTGAAGTGGACTTCAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAGAAC
 TGGTCTATACAGCTGAGGAGAGTTTGTGGGAGCTCAGAAATTTGTGACCACTGGAGCTGGAGATAGAAT
 ATGACTCTCTTGTGATAGAAAGCTTGAGACACTAGACAAAAAATGTCCTTGCATTCGCCGAGAATCTGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCTCTAAAGATCAAAACACCCCTCTGCTCCACCCTCTCCCACTC
 CAGGGAGCTGTGGTCATGTGTGTGTGGAACATCAGCAAAACCGTCTGTGTTTCAGCTCAACTGGAGAGGTTT
 TCTTATCTATATGTTGCTTGGGGTAGGGATTACTCTCCCAGCATCCAAACAAAGGACTGTATTGGGTGGCGC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGATTAACTGACCACCAACAGGATTGCTGTGACTCAAACCTCTCCCTAA
 TGCTGCCATATAAATACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAAGCCCTCATGGTATGTGGGGTTCT
 GTATGCCACCCGACTATGAACACCAGAACAGAGAGATTTTTACTATTATGACACAAACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACATAACCCCTTTTGACAGAAA
 CTTTATGTTCTATAACGATGTTTACCTTCTGAATTATGATCTTCTGTCTGCGAAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGTTGAAAGAGAAATGTTTGTGAAAAATAGTCTTCTCCACTTACTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTTCAATTTGCAGCAATGTTTAGTGCATAGTCTACCACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCCTTTCAGGCGCATTTTGCAATAAGTCTGTCTAGGGTGGGA
 TGTTCAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCCTACTGTGAGGAGGCTTCACTAGAGCCCTTAATTA
 GGAATTAAGGAACCTAAACCTAGTATGGGCTTAGGGATTCTTTGTACAGGAATATTGCCCAATGACTAGTC
 CTCAATCCATCTAGCACCACTAATTTCTCCATGCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAATCTCCTCACTTTTTTTCCCTCACTAGCACTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATCTACATCTGTAAGTGCTGAGTTTATGGAGAGAGCCCTTTTT
 ATGCATTAATTTGTACATGGCAATAATCCAGAAGGATCTGTAGATGAGGCACTGCTTTTTCTTTCTCTC
 ATTGCCACCTTACTAAAAGTCAGTAGATCTTACCTCATACCTCTCTTCCAAAGCGAGCTCAGAAGATTAG
 AACCAGACTTACTAACCAATTTCCACCCCAACCCCTCTACTGCTACTTTAAAAAATTAATAGTTTT
 CTATGGAAGCTGATCAAGATTAGAAAAATTAATTTCTTTAATTTCAATTGACATTTTATTTACATAGCTCA
 AGACTATAAGAAAACTGATGGCAGTGACAAGTGTAGCAATTTATTTGTTATTAAGAAGCTTGAGCATA
 TGTGCACTTATGAGTGTATCAGTTGTTGCTATGTAATTTTTGCTTTTGTTTAAGCTGGAATCTGTAAGAAAT
 GAAAAATTTAATTTTTTTCTAGGACGAGCTATAGAAAGCTAATGAGAGTATAGCTTAATCAGTGCAGTAGT
 TGGAAACCTCTGTGGGTATGTGATGTGCTCTGTGCTTTGAAAGACTTATCATCTAGCTTTGTCTATTTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTTACTCCCCCTTTTAAATAAATGAT
 TAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

CTAAGAGGACAAGATGAGGCCGCCGCTCTCATTTCTCCTAGCCCTTCTGTTCTTCTCTGGCCAAAGCTGCAGGGG

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSFPFVDSFSSSSSSRSGSSSSRLGS
GGSVSQLFSNFTGSVDDRGTCCQCSVSLPDTTFPVDRLERLETAHVLSQLKEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGLYWVAPLNTDGRLLLEYRYLNTLD
DLLLYINARELRITYGQSGTAVYNNMNYVMYNTGNIARVNLTTNTIAVTQTLNPAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGLYATRTMNTREEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFQKLYVYNDG
YLLNYDLVSVLOKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCCTGCTCTTGTGACGTTTGTGGAGATGGGAGCGTCTGGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTGTGTGAAGTGCCCCGTGTTTGCATGCCGATGCTGCTAGTGGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACCTTTTCTTGCTTGTGGAGTATGTGTAGCTTG
 TGTAACTTGTATACAGGAATGGAAGAACAACCTGAATAAGATTTCCTGGATTTTGTGAGAATG
 AGAAAGCTGTTGTCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAGAGATGACGTGA
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCGACAATTGCACATTA
 TTATTGGGGCATCTTCATCCAGAAGGAACCTTTACAACTGTGTGGTTTTATGTAGGCATG
 GCAGGTGCCCTTTGTTTCATCCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCGAATTATCTGCTGTCTTTAGTTGCTATCGTCCTGTCTTTGTCTAC
 TACACTCATCCAGCGAGTTGTTCCAGAAAACAGGCGTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACCTGCCAAAAATCCAAGATCACAACCAAGATCTGGTT
 TGTACAGTCTTCAGTAATTACAGTCTACACAATGATTTGACATGGTCAGCTATGACCAAT
 GAACCAAAAAAATTGCACCCCAAGTCTACTAAGCATAAATGGGCTACAATACAACAAGCAC
 TGTCCCAAGGAAGGGCAGTCACTCCAGTGGTGGCTGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGGTTGTGTGATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAA
 CTGACTCTAACAAGTATGAATCTACATTAATAGAAGATGGTGAGACTGAAGATGAGGATG
 ACTGGAGGATGGGACAGTGTTCACCGAGCTGTAGATAATGAAAGGATGGTGTCACTTACA
 GTTATTCTCTCTTCACTTCACTGCTTTTCTGGCTTCACTTTATATCATGATGACCTTTACC
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAGTCACTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCGATTTGGATTTGGCATCGTGTGTATGTTTGGCACTCGTGGCACCCTTGTTC
 TTACAAATCGTGATTTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCAGTCTTGATTTATG
 TTATTGAAAAACAGTATCCCAACTTTTGTAAAGTTGTGTATGTTTGTCTCCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTTTCTACCAA
 GTGCATTGATATGTGAAGTAGAATGAATTCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAAGATGGCCATTATTTGGGCTTATCTCTGCTCTATAGTTTGTGAATGAGAGTAAAA
 ACAAAATTTGTTTGACTATTTTAAAAATTATATAGACCTTAAAGCTGTTTGTAGCAAGATTAAA
 GCAAATGTATGGCTGCCCTTTGAAATATTTGATGTGTTGCCCTGGCAGGATATGCAAAAGAC
 ATGGTTTATTTTAAAAATTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTATCCCTGTATACGGAATTTACACAGGTAGGGAGTGTTAGTGGCAATAGTGTAGG
 TTATGGATGGAGTGTCCGTACTAAATGAATAACAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAACCTGTTTGGTGTGTTTAAACCTCATGAAGTATGGGTTCA
 GGAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTGAAGGATAATCATGGGTTAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTGTAGTTTGGGCCAGCACGCTAGCTCACCCTT
 GGTAAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTGAGCCAGGAATTCAGACCA
 GCTTGGCACAATGGTGAACCTGTCTATAAAAATAATCTGGCTTTGAGCATATGCCTGTGGTC
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGTTGCGATGAGCAAGTCA
 CGTCACTGCACCTAGCTGGCAGAGTGAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCAAAATTTGACAGGAAGGAAGTAACTGCAAAACCACTAGTCTTAGTAGGTACTTAT
 ATAAACCTAGTCCAGTCTCTCATTAAAAAATGAAGACATGAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAATTTCAAGTTGGCCAATAATAGCATTCTCTGACATTTAA
 AATATTTCTATTCAAATACATGCATATTGATTTACACCTCATACTGTGATTAATTAATGT
 GATGTGAATGCTGGTGTACAGCATGACCCATAACAGGTCAAGAATGATGGAATGAGCTTTT
 AGATAAATCTCTGCTTATAGTATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATCTAAATGAAATATATAGATTATGTAACCTTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTAGTATTATGATGTGTCACTAGTGTCTAATGAGCTTTTAAATCTCAAAAT
 TCTTTCTTTAAAAATTTTAAATGATGAATGGAATATAACATTCAGCTTAATCCCCAAC
 TTATCTGTGTGTAGACATTGTATCCACAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

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MGSVLGLCSMASWIPCLCGSAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCAVCMILPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFLGLAMFYLLLSLLMTKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFPIPEGTFTTVWFVVGMAGAFCPILQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAAALSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPSRGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLISIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNQVKNLTLSDESTLIEDGGARSDGSLDGGDDVH
RAVDNERDGVITYSYFFHFMLFLASLIIMTLTNWSRYEPSREMKSQWTAVWVKISSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAATGGAT
TTTGGTTCCTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAAG
GTGTTGTCCCTTGTAACATTTTGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAAC TAGATTGATCTATGCACCT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTCGATT TTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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10000 100000 1000000 10000000 100000000 1000000000

1980 100 1119

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTGCGGCGCGCGCGGCTCTCCAAT
 GGCAATATTGTGTGCTGGAGGGGAGCGCAGGCTTCGGCAAAAGGCAGTCGAGTGTTCGACAGCCGGGGCGAG
 TCCCTGGAAGACAGATAAAAAGAAACATTTATTAACTGTCTATTACGAGGGAGCGCCGGCGGGGCTGTGCG
 ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAGAAAGAAAGCGGAAAGAGGCAGATTCAC
 GTCTGTTCCAGGCAAGTGGACCTGATCGATGGCCCTCTGAATTTATCAAGATATTTGATTTATTAGGATGCGC
 CCCTGGTTTGTGTGTACGCACACACAGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCG
 TGGGCGAATCCCACTGTGTTTCACTCTCCGCGAGGCGAGCAGAGCAGAGTGTGTGCAATCTGCGAGTGC
 AAGAGGGACAGGGGAAAAAGAAACAAAGCCACAGACGCAACTTGAAGATCCCGCATCCCAAGAACACACAGAT
 CAGCAAAAAAAGAAAGATGGGCCCCCGAGCCTCGTCTGTGCTTGTGTGCGCAACTGTGTTCTCCCTGCTGGG
 TGAAGCTCGGCTCTCTGTGCGACCCGCGCTGAAAGGAGGTTTCAGAGGACCGCAGGAAACATCCGCCCCA
 ACATCATCTCTGTGTGTGAGCGGACGACAGGATGTGAGCTGGGTTCCATGACAGGTGATGAACAAAGACCCGGCGC
 ATCATGGAGCAGGGGCGGGCGCACTTCATCAACGCTTCTGTGACCAACCCATGTGCTGCCCTCAAGCTCTCT
 CATCTCTCACTGGCAAGTACGTCCACAACACACACCTACACCAACATGAGAATGCTCTCGCCCTCTCTGGC
 AGGCACAGCAGAGAGCGCACCTTTGCGCTGTACTCAATAGCACTGGCTACCGGACAGCTTCTTCGGGAAG
 TATCTTAATGAATACAAACGCTCTTACGTGCCACCCGCTGGAAGGATGGTGGTGGGACTCTTAAAAACTCCCG
 CTTTTATAACTACAGCTGTGTGCGAACGGGTGAAAGAGAGACGCGCTCCGACTACTCCAAGGATTAACCTCA
 CAGACCTCATCCCAATGACAGCGCTGAGCTTCTCCGACGTCCCAAGAGATGTACCCGACAGGCGAGTCTCT
 ATGGTCATCAGCATGACGCGCCCCAGCGCTGAGGATTCAGCCCAACATATTACGCTCTCTCCAAACGC
 ATCTCAGCACATCAGCGCGAGGTACAACTACGCGCCCAACCCGGACAAACACTGGATCATGGCTACACGGGGC
 CCATCAGCGCCATCAGATCGAATTACCAACATGCTCCAGCGGAAGCGCTTGCAGACCTCATGTCTGGTGGAC
 GACTCCATGGAGACGATTTCACACATGCTGGTTGAGACGGGCGAGCTGGACACACAGCTACATCGTATACACCGC
 CAGCCAGCGTTTACCACATCGGGCAGTTTGGCTGGTGAAGGAAATTCATGCCATATGAGTTTGAATCAGAGG
 TCCGCTCTCTACGTGAGGGGCCCCACGCTGGAAGCGGCTGTCTGAATCCCCACATCGCTTCAACATGTAGCTG
 GCCCCCCACTCTGCAGCATTCAGGCTTGGACATCTTGGGATATGGACGGGAAATCCATCCTCAAGCTGCT
 GGACAGCGAGCGCGCTGAATCGGTTTCACTTGAAGAAAGATGAGGCTGTGGCGGAGCTCTCTTGTGTGG
 AGAGCGCAAGCTGTACACAAAGAGAGACATGACAGGTGGAGCGCCAGGAGGAGAACTTTCGCGCAAGTAC
 CAGCCTGTGAAGGACCTGTCTCAGCGTGTCTGATACAGCAGCGGCTGTGAGCAGTGGGACAGAGTGGCAGT
 TGTGAGGAGCGCCACGGGAAGCTGAAGCTGCATAAGTCAAGGGCCCATGGCGCTGGGCGGACAGGACCC
 TCTCCACCTCTGTGCCAAGTACTACGGGACGGGACGAGGCTGACACTGTGACAGCGGGGACTTCAAGCTC
 AGCCTGGCGGAGCGCGGAAAAAATCTTCAAGAAAGATACAAGGCCACTATGTGCGCAAGTCTCGCTCCATCG
 CTCAGTGGCCATCGAGGTGAGCGCGGCTGTACACCTAGGCGCTGGGTGATGGCGGCCACCGGAAACCTCA
 CCAAGCGCACTGAGGCGGCCCCCTGAGGACCAAGATGACAAGCATGTTGGGACTTCACTGGCTGTGAGG
 CTTCGCGACTACTCAGCGGCCAACCCATTAAAGTGACACATCGGTGTACATCTTAGAAGACGACAGCATGCCA
 GTGTGACTGTGACCTGTACAGTCCCTGCGAGGCTGGAAGACCAAGCTGCACATGCACATGCACAGATTTGAA
 CCTCGAGAACAAATTAAGAACTCTGAGGGAAGTCCGAGGTCACTGAAGAAAAAGCGGCGCAGAAGATGTGAC
 GTGTACAAAATCAGTACCCACCCAGCACAAAGGCGGCTCAGGCACAGAGGCTCGAGTCTGCATCTCTTTCAG
 GAAGGCGCTGCAAGAGAAGGACAGGTGTGGCTGTTCGGGAGCAGAAAGCGCAGAGAAACTCCGCAAGCTGC
 TCAAGCGGCTTGACAGAACACGACAGCTGCAGCATGCGAGGCTCAGCTGCTTCACCACGACACAGCAGCTG
 CAGAGCGGCGCTTCTGGACAGCTGGGCGCTTCTGTGCTGCACAGCGCGCAACATACACGTAAGTGGTCACT
 GAGGACCATCAATGAGACTCACAATTTCTCTCTGTGAATTTGCAACTGGCTCTCTAGAGTACTTTGATCTCA
 ACACAGACCCCTACAGCTGATGAATGCAAGAACACTGGACAGGAGTGTCTTCAACAGCTACTGAGCTACAG
 CTCTATGAGCTGAGGAGCTGCAAGGTTTACAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAG
 AAGCTATGAGCAATACAGCGCTTCAAGCTCGAAAGTGGCCAGGAATGAAGAGACCTTTCTTCAAACTCTG
 GACAACTGTGGGAAGGCTGGGAAGTTTAAAGAAACACAGAGTGGACTCCCAAAACATAGAGGCATCACTGA
 TCTGACAGGCAATGAAGAACATGTGGGTGATTTCCAGCAGACTGTGCTATTTGGCCAGGAGGCTGAGAAGC
 AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACAGCAGGAGCAGAGATACCTCAGGAAGCTC
 ATTTTTCGCCCTGCTTTGCTTTGGATTATACCTCACCAGCTGCACAAATGCAATTTTTTCGTATCAAAAGT
 ACCATCAACCTCCCCAGAAGCTCACAAAGGAAACGGAGAGAGCAGGAGGAGAGATTTCTTGGAAATTTT
 TCCCAAGGGGAGAGTCAATTTGGAATTTTAAATCATAGGGGAAAGCAGTCTGTTCTAAATCCTCTTATTTCT
 TTGGTTTGTACAAAGAGGAACATAAGAAGCAGGACAGAGGCACTGGGAGGCTGAAACAGCTGACAGAGC
 TTTGACATGAGTCAGTGAAGAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCTCTGAAAGAA
 CTGCCTTCTATGTATATGTGTACTATTTACATGTAATCAACATGGGAACTTTAGGGGACCACTATAAGAAAT
 CCAAATTTTCAGAGTGGTGGTGTCAATAAACGCTCTGTGGCAGTGTAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLGSSAFLSHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQ
 VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
 RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
 YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
 SYNYAPNPDKHIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
 YIVYTADHGHHIGQFGLVKGKSMPIEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
 AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
 FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKHKCKGPMRLGGSRALSNLVPKY
 YGQGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAQ
 PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLDLYKS
 LQAWKDKHLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
 HPFRKGLQEKDKVWLLREQKRKKLRLKLLQNNDCSMPLTCTFHDNQHWTAPFWTLG
 PFCACTSANNNTYWCMRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
 HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPPSSKSLGQLWEGWEG

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AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCACATGCTGGGCCCTCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCGCGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTACC
 ATCACCGTCATCTTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACAC
 CCCCGCCACACCCTCACCACCTCCACCACCACCACCACCACCACCACCCACCGCCACCATCCCCGCCA
 CGCTCGCTTGAGGCTGCTGTGCGCCGGTGCCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTCAGTGTACTCCAGTGAGCCCCAGAAATG
 ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
 ATCAGGCTGCTGCAGGCCTGTGCGGGCAGGGCAGCTGGGAGAGGCCCTGAGAATGTCCTTTT
 GTTTTGGAGAGGCATGTGAGGCTGCACAGTCAATTCTACGTTGCCCTTAGTCCAAGAAAT
 AAAAAACCATAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQWPWPF
RRGHLGIFHHHRHPGHVSHVFNVLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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GGCGGCTGCTGAGCTGCCCTTGAGGTGCAGTGTGGGGATCCAGAGCCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTA CT CAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGTTGAGACTGGGCGCTTTTCTACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAAGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATCTGTCCATCTGGCTGGCTACCCGCCG
TGTCATCTGCTGCTTGGACACTACCTACAGGAGCGGAAGCTGTGTGCCATCTCTCGGCTGG
AGATCTACAGGAAGACAGCATGCTCAATTTCACTGTGCCCACTGGCAGCGCAGGAGACTCTTAT
GTGCTTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAGGAGTAACCCC
ATGGCCTGACCTCTCTGCAGTGCAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCCTCCTTCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACACGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGTGAGCTTCCAGGACCCAGAATAAGGCCAATGATTACTTGTTTCACTGGAAAAAA
AAAAA

MSDLLLLGLIGLTLTLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyETGR
LFTESCSISPKLRSIAVYYDNPHMVPDPKCRCAVGSILSEGESPSPELIDLYQKFGKVFVS
FPAPSHVVTATFPYTTILSIWLATRVRHPALDITYIKERKLCAYPRLIEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDGDGTRSEHSYSESGASGSSFELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCGGCTCCCT
 GCCCCGCGCCAGT**CATG**ACCCCTGCGCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESFVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

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CCCGGGAACGTGTTCTCTGGCTGCCGACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCC GCGCC CAGTCATGACCC TGC GCCCT CACTCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGT GCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAAC TACTGGCTAAAGCTGGTGAAGGGCATT TTGCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCTCTGGGCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGCAAGTGCACGGAAGAGAAACGAAACAGAGCAAAAAGAAATAATA
ATAATAAAATTTAAAAAACTTA

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACAGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACGGGGATTTCCACCATTCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCTGGGCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAATTTTAAAAAACTTAAAA

CTGCTGCATCCGGGTGCTCGAGGCTGTGGCGTTTTGTTTTCTTGCTAAAATCGGGGAG
TGAGGCGGGCCGGCGCGCGACACCGGCTCCGGAACCATGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGTCTCGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCATTGCTGCTGGTGACTATTTTTACAGGCTGGTGGAT
TATCATAGATGCACTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTTATAGCAACCATAGCCTTCTTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGCTGGGTCAACAGGTGCTCGCATTTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGATTTTTCCAGAATGCCATCTATT
TTTTGGAGGCTGTTTTTAAAGTTTGGCCGACGAAGACTTATGGCAGTAGCAACATCTGAT
TCTCCACAGCACAACAGCCCTGCATGGGTTTGTTTGTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACCTTAACAACAACCAAAAAATCTATTGTGGTATGCACTTGATTAACCT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
TGTA AAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTAATCAATGTGGT
CTCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAAAATATCCGTGG
TCAAAATCTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGCTCTCCGCTGTGCCTCTCATT
CCAAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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TGGACGGACCTGAAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAACTACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGAGNTGTTATTTATCCACCATGAAAGATTTC AACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCGATATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTGTGTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTCGATCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTATAAGAAAAGACATAGTATATCTACCTGGAATGNTGTATTTTCCAGAATGCCTT
ATCTTTTTTGGAGGGCTGTTTTTTAAGTTTGGCCGCATGAAGANTATGCGCAGTG

GGACACCGGGTTCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAACGCAATANTATTGCTTT
CCATTGCTGCTGTGTACTATTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
CTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGGTTTCATGTTGGCCTTTGGATT
GTGATTGNATTCATGCGGATCTCTCTGGAGGTTATGTTGCTAAAGAAAAGACATAGTAT
ACCTTGGAAATNCTNTATTTTTCCGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

TGGGTTTATGAGGTTT

FIGURE 62

GGGAGGCTGTGNCCGTTTGTGTTTNTTGGCTAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCGGCGGT**ATG**TGGCTTCCGCTGGTGTCTGCTCCTGGCTGTGCTGCTGCTGCGCGTCC
 TCTGCAAAAGTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
 AAACGGCCCCAGCGCCCTGGTAACCTGACAAGGAGGCCAGGAAGAAGGTCTTCAAAACAAGC
 TTTTTCAGCCAACAAGTGGCCGAGAAAGCTGGATGTGGTGGTAAATTTGGCAGTGGCTTTGGGG
 GCTTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTCTGGAAACAACAT
 ACCAAGCGAGGGGGCTGCTGTCTATCTTTGGAAAGAATGGCTTGTAAATTTGACACAGGAAT
 CCTATTACATTTGGGCTATGGAAAGAGGGCAGCATTTGGCCGTTTTATCTTGGACAGATCACTG
 AAGGGCAGCTGGACTGGCTGCCCTCTCTCTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC
 AATGGCCGAAGAAGGATACCCCATGTACAGTGGAGAGAAAGCTACATTAGGGGCTCAAGGA
 GAAGTTTCCACAGAGGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
 GTGGAGCCCCCTATGCCATCTGTGTGAATTTCTCCCATTTCCCGTGGTTCACTCTCTCGAC
 AGGTGTGGGCTGCTGACTCGTTTCTCTCATCTTCTTCAAGCATCCACCAGAGCCTGGCTGA
 GTCTCTGCAGCAGCTGGGGGCTCTCTGTAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
 CTTAGGCTGTCAACCCCCAACACAGTGCCTTTTCCATGCAGCGCCCTGCTGGTCAACCATAC
 ATGAAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTTGCCCTCCACACCATCCCTGT
 GATTACGCGGCTGGGGGCGCTGTCTCTACAAAGGCCACTGTGCAGAGTGTGTGTCTGGACT
 CAGCTGGGAAGGCTGTGGTGTCACTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
 CACTCTGTGTCTCCAACGCAAGGACTGTCTCAACACCTATGAACACCTACTGCCGGGGAAGCG
 CCGCTGTGCTCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCGGCTTAGGCATGACCT
 CTGTTTTCTACTCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCCTCCACCACTACTAT
 GTTTACTATGACACGGACATGGACACGGCGATGGAGCGCTACGTCTCCATGCCAGGGAAGA
 GGCTGCCGAACACATCCCTCTCTCTCTCTCTCTTCCCATCCAGCAAAAGATCCGAGCTGGG
 AGGACCGATTCCCGAGGCGGCTCCACCATGATCATGCTCATACCCACTGCCACGAGTGGTT
 GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCACTGACTATGAGACCTTCAAAAAGTCT
 CTTTGTGGAAGCTCTATGTCTAGTGTCTTGAAGTCTTCCCAAGCTGGAGGGGAAGGTGG
 AGAGTGTGACTGCAAGATCCCCACTCACCAACCAAGTCTATCTGGCTGCTCCCCGAGGTGCC
 TGTACGGGGCTGACCATGACCTGGGCGGCTGCACCTTGTGTGATGGCTCCTTGAAGGCG
 CCAGAGCCCCATCCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTGG
 GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGAC
 CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAAT**TAG**TTCCATCAGGGAGG
 AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
 CATTAAGTTCTTTGACGATATAAGCACTCTAATTTGGTTCTGATGCTGAAGAGAGGCTTAG
 TTTAAATACAATTCGGAATCTGGGGCAATCGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
 TCTTTAGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTTGATG
 TCTCATGACGAGCGGCGCTCTGCATCCCTCACCATGCCTCTCACTCACTGATCAAGCGGA
 ATATTCCATCTGTGGATAGAACCCTTGGCAGTGTGTGACGCTCAACCTGGTGGGTTCAGTTCT
 TGTCTTGAGGCTTCTGCTCTATTCTTTAGTGCTACGCTGCACCTTCTACACTGTCAAGG
 GAAAAGGGAGACTAATAGGGCTTAACTCAAAACCTGGGCGTGGTTTGGTTGCCATTTCCATA
 GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCACTGGCTCTTCAAGGGACAGGAAT
 GCGTGTGCTGTGGCAGTGTGGTTCTTGAGAGTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
 GGCTGCATGTGAGATGATCATATCCAATTATATGGAAGTCCCGGGTCTGTCTTCTTATCA
 TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACTGAGCCTCAATCAAGC
 CTTATCCCAAAATACACAGGGAAGGTGTGGGTAAGGAGGGAAGTGCATCAGGATCAGGGCA
 TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTCGAGGGCATCCAGCCAAGGG
 CACAGCAGGGGACAGTGCAGGGAGGTGTGGGTAAGGAGGGAAGTGCATCAGGATGCTGGT
 AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTGAGTTAATAGCATATGTGGGG
 TTAGACAGTGGTGAATGCAAGCTCAAGGTTTGAAGAAATGACTTTGCTAGTTATGCTTTG
 GTATCAGACATACGAAGGTCTCTTTGTATGTTCTGTGTTAATGTAACATTAATAAATTTATTG
 ATTCCATTGCTTTAAAAA

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[illegible]

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTTLTSDSESVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESNPENKDYEEPKVKRKALTAIEGTAHG
EPCHFPFFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWFCEETEEAAKRRQMGEAEMM
YQTGMKILGNSNKKSQKREARYRLQKAAMNHTKALERVSYALLFGDYLPQNIQAAREMFEK
LTEEGSPKGTAKGLFASGLGVNSNSQAKALVYTFGALGGNLIAHMLVNSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
 GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGACCTTCCT
 GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
 CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTGG
 TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
 CCACCGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
 GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
 TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCATTCT
 GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCTCTGTAAATGGG
 TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADI PDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

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FIGURE 69

GCGGCCCGCCGAGACCGGGGCCGGGGCGCGGGGCGGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGACCGCGCGGGCCCGGCCCTGACCCCGCGCCCGCCCGCTGAGCCCC
 CCGCGCGAGGTTCGGGACCGCCGAGATGACGCGCGAGGCCCTGTGCTGCTCCTGCTGCGCG
 CGCTGCTGCTGGGGGCCCTTCCACCGCGCGCGCGCGCGCGGAGGCCCGCCCAAGATGCGCGGAC
 AAGGTGGTCCACCGGACGTGGCCCGGCTGGGCGCACTGTGCGGTGCAATGCCAGTGGATGGA
 GGGGGACCGCGCGCGCTGCGCGAGGGCTGAAGGTGAAGCAGTGGAGCGGAGGATGCGGGC
 GTGTAGCTGTGTAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCTCGTCTGT
 GCTGGATGACATTAGCCAGGGAAGGAGCCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCAGCGCGCTGGGTAGCTCCGTGCGGCTCAAGTGGCGGGCAGCGGGCACCC
 TCGGCGGACATCACTGGATGAAGGACGACCAGGCCTTGACGCGCCCGAGAGGCGCGTGAGC
 CCGGAAGAAGAAGTGGACACTGAGCTGAAGAACCTGCGGCCCGGAGGACAGCGGCAATAC
 ACCTGCCCGGTGCTGAACCGCGCGGGCGGCATCAACGCCACCTACAGGTGGATGTGATCCA
 ACCTGCCCGGTTCAGAGCCGTGCTACAGGCACGACCCCGTGAACACGACGGTGGACTTCG
 GGGGGACACAGTCTTCCAGTGAAGGTGCGCAGCGACGTGAAGCGGTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGGCCGAGGGCCGCCCAACTCCACCATCGATGTGGGGCGGCCAGAA
 GTTTGTGGTGTGCTGCCACGGGTGACGTGTGCTGCGCGGCCGCGCGCTCCTTACCTCAATAAGC
 TGCTCATTCACCGTCCGCGCAGGACGATGCGGGCATGTACATCTGCTTGGCGGCCAACAC
 ATGGGCTACAGCTTCCGACGCGCTTCTTCACTGCTGCTGCGAGACCGAAAACCGCGAGGCC
 ACCTGTGGCGCTTCTGCTCTCGGCCACTAGCTTGGCGCGGTGGTCACTCGGCATCCGAC
 CGCGCGCTGTCTTCACTTGGGACCCCTGCTCTGTGGCTTTGCCAGGGCCAGAGAAGCGC
 TGACCCCGCCGCTGCGCCCTCCCTGCTGGGCGCGCCCGCGGGGAGCGCGGACCGACCG
 CAGCGGAGACAGGACCTTCCCTCGTGGCGCGCCTACGCGTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGTGGGTCTTCGGGACGCCCGCCAGCACTTACTGGGCGCAGGCCAGTGTGCTGGC
 CCTAAGTTGTACCCAACTCTACACAGACATCCACACACACACACACACACTCTCACAC
 ACACCTACACAGTGGAGGGCAAGGTCCACGACATCCACTATCATGTGCTAGACGGGACCGT
 ATCTGCAAGTGGGACGGGGGGCGGCCAGACAGGCAGACTGGGAGGATGGAGGACCGAGGT
 CGACAGCAAGGACAGGGGACCATGGCGAGGAGGAATGGCCAGCACCCAGGCGAGTCTGTGTG
 TGAGGCAATAGCCCTTGGACACACACACACACACACACTACCTGGATGCACTGTATGCAC
 ACACATGCGGCACACGCTGCTCCCTGAAGGCACACGTAACGACACGCACTGACAGATATG
 CCGCTGGGACACAGGATATGCTGCTGGACGACACACGTCAGATATGGTATCCGGACACA
 TACAGGACATGCTGCTGAACATACACACGCAACCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACAGGATATGCTGCTGGACGACACACGTCAGATATGGTATCCGGACACA
 CAGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTTGACACACATGACAGG
 ATATTGCTGGACACACACACACACACACGCGTGCACAGATATGCTGCTGGACACGACAC
 ACATGACAGATATGCTGCTGGACACACACTTCCAGACACACGTCGACAGGCGCAGATATGCT
 GCCTGGACACACGAGATATGCTGCTAGTACACACACACGACAGATATGCTGCTGGGACAC
 ACACACGATGACAGATATGCTGCTGGACACACACGCGCAGATATGCTGCTGGATACACG
 CAGCAGACATGACAGATATGCTGCTGGGACACACTTCCGGACACACATGACACACAGGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCTTCAACACTCACACAGTGCAGAG
 TATTGCTGGACACACATATGTCAGATATGCTGCTGGACACACACAGTGCAGAGTA
 TGCTGCTGGACACACGACGACGACATGACAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGACACACAGGTGCAGATATGCTGCTGGACACGCGAGACTGACGTGCTTTTGG
 GAGGTTGCGGTGAAGCCTGCGTACGTGTCGCGTGGGCTCATAGTTGATGAGGACTTT
 CCCTGCTCCACGCTCACTCCCAACTCTGCGCGCTCTGTCGCCGCTCAGTCCCCGCTC
 CATGCCCGCTCTGCTGCTGGCTTGGCGGCTATTTTGGCCACTGCTTGGTGGGCGGAGG
 AGTCCCCCTACTGCTTGGGCTGGGTTGGGGGACAGGAGCCCAAGCCTGAGAGGCTGGAG
 CCATGCTAGTGGCTCATCCCGAGTGCATTTCCCTTGACACAGAGAAGGGGCTTGGTA
 TTTATTTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGAC
 TGTGGTCTCTCTGGGGCGGGACCCGCGCTGGTCTTTCAGGCACTGCTGATGACCAACCC
 GTCCAGGCGACACACCCCGACCCCACTGTGCTGGTGGGCGGAGATCTCTGTAATTTTA
 TGTAGAGTTTGGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACAAAA

FIGURE 70

MTPSPLLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDISP
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA RPVGSSVRLKCVASGHRPDPITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRS DVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWVPVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGSFAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSHSHVEGKV
HQHIHYQC

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FIGURE 71

CCAGCTGAGGAGCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCACGGGGACCGGATTCACAGAGTC
 AGTGAATCTCTGTAAGACCCACATCTACTCTTGGCCAGCTTCCACGGGCTTGGGGGAAAGATGTTGGGGGACCA
 AGGCTGGGGTGTCTTCTCTCTGGTCTGGGAAGTCACATCTGTGGGAGACAGACGATGCTCACCCAGTCA
 GTAAGGAAGTCTCCAGCCTGGGAAGAAGAACCACAGCATCTTTGCCAAGCTGCGCCACACCTGGAGAGCCCTGG
 TGAGTGACACACATGCTTCAACATTCGACTTCCAGGCGGGAAGGCGACTATGAGCGGCTGGACGCCATTCGCT
 TCTACTATGGGACCTGTGTATGCTCCGCTGCTGAGGCTGAGGCGCTGAGCACTGCTGAGCACTCCGCGGCT
 AGCATGCGCAGCTGCTGTATGCTAGTCCCGTGAGGGTTTCTGCTGCTTCAACAGGAGGACCGCGCTGGCCA
 GAACGTCTCTAATTACACCGTAGCTTCTCTGCCCCACGAGGATCCCTGGCGGACAGACAGAGCGCATCTTGGA
 GCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCTTGGTGAGACTGGGGTCCAGACTCGCACACGATTCCTTGC
 TTGGCAGAGATCGCTTCCGCTGTGAGTGGGCCAGCGAAGAGGGTTCAGACTGCATGGGCGAGCATGTGACAGC
 CTGTGACCTGACCTGCCAATGGGCGAGTGAATGCTGACTGTGATGCTGCTGATGTGGCAGGATCTCATGCTTC
 ATGGGCTCTCCCTTCCGAGAGTGGCCAGCTCAGGGCTGCTATCTCTCTGACAGAGAGCGCGATC
 CTGCTGACCCAGACAGACAGTGTGGGAGATTCCGAATCCCTGGCTTGGCCCTGATGCGCAAAAGCATCTTGAA
 GATCAACAAGGTCAAGTTTGGCCCCATTGTACTCAATGCCCAAGACTAGCTGAAAGCGGCCACCATCAAGG
 CAGATGTTTGGAGGCGACAGACTCCATACATGGTGATGAACCTGACACAAAGCAGGAGAGCTGGGCGAGCG
 GTGCTCTGCTGTGCTGTGAAGGCCACAGGGAAGGCCAGGCAGACAAGTATTTTGGTATCATATGACACCATTTGCT
 GGATCTTCTCTCTACAAGATGAGACAACTGGTCTGAGGAACCTGCAGCAGCAAGGCTGGGCGAGTATCT
 TTTGCAAGGCCCAGAGTGTGCTGGGCTGTGAATCTGCTGACAGCTTGTGTCACAGCTGTGATGAG
 ACTCTTGTGAACCGCTTCTGAGAGCTATCTTATCCGCTGCCCATGATTCGTTTTCAGAAATGCCAACCACT
 TTCTTACTATGCTGGGAGCGCTGCCCTGTTAAGACTTGTGACGGGACAGAGGATGAATGGGATCAGGTGGCGTG
 ATGCTGTGCGACATGCTGTGGTCTTCAACAGCAGGGAAGGAGGATCCAGTGCAGTGGCTACACGCTACCC
 ACCAAGGTGGCAAGGAGTGCAGCTGCCAGCGGTTGACGGAACCTGGAGACTGCTGCGGGGCGGCTGTGACTGC
 TGCTGACATTTGGGGAGCCCATGCGCTTTGGCCATGTGTACATGGGGAACAGCGCTGTGAGCATGCTGGCTACA
 AGGCGACTTTTCCCTCATGCTCCCGAGGACTGAGAGGCTGTGCTCATGATTTGTGACAGGCTGCAGAG
 TTTTGTCAACACACCAAGGTGCTACCTTTCAACAAGAAGGGGAGTGCCTGTTCCATGAATCAAGATGCTTCTG
 TCGGAAGAGCCCATCATTGTGAAGCCATGGACACCAACATCATCCCCCTGGGGGAAGTGGTGTGTGAAGAC
 CCATGGCTGAATGGAGATTCATCCAGGAGTTTCTACAGGCGAATGGGGAGCCCTACATAGGAAAGGCTGAAG
 GCCAGTGTGACCTTCTGGATCCCGGATATTTTCCACAGCCAGCTGCCAGACTGACCTGAACCTTCATCAA
 TGACGAAGGAGCACTTTTCCCTTCCGACTATGGCATTTCTCTGTGACTTACAGATGAGGTCACTCCAG
 AGCCACTTAATGCTGGCAAACTGAAGTCCAACTTGAATGACCTGACAGTCCAGATGCCAGAGCATTCACAG
 GTGAACCTCTGCTCACTCAATCAGACACAGGGCTGTGGGAGGAGGGAAGTGTGTTCAAATTTGAAATCAAAG
 GAGGAACAAAGAGAGAACAGCACTTCTCTGGTGGGCAACCTGGAGATTCGTGAGAGGAGGCTCTTTAACTCTG
 ATGTTCTCTGAAGCAGGCGGTGCTTTGTTAAGGTGAGGGGCTTACCGGAGTGAGAGGTTCTTCTGCTAGTGAGCAG
 ATCCAGGGGGTGTGATCTCTCGTGATTAACCTGAGAGTGGCTTCTGTGCTCAACCTAGGCGCTGGGCTGGG
 CCGCTTTGACAGTGTGATCAGCGGCCACAGGGGCTGTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT
 CTTACTCTGCTATGCTGTGACAGGCTGCTGCTGGGAGGAATGCAACAGCTGGAGTCTTCTCTAAATTCAC
 CCAAATGCAATTTGGGCTCCCTCAGCCCTATCTCAACAGCTCAACTCCCTGGGACCGACATCAGGATGCCAG
 GGTAAAAAGCAGCTTTCCAGATTAGCATGGCCAGCCAAAGGCCAACTCAGCTGAGGAGAGCATGGGCCCA
 TCTATGCTCTTGAAGACCTCCGGGCTATGTGAAGAGGCCAACCCAGCTGACGCCACTTCGCTTCTACCGATT
 GAGGGGAGTCGATGACTACACACACAGTCCCTTCAACGAAGATGACCTATGAGCTGGAATCAAGCATCTG
 GGCTGCTGGCCAAAGCATGATGATTCAGGCTGCTATGATGAGTGAAGATTCTGGGCGACTGAGATGAT
 ATTCGCTATCCGCAACATGGGGGCACTCATCGCGGACATGGGAGCTGTATGGAATCCGAGATGTGAGG
 AGCATCTGGGACAGGACCGCCCAATGCTCAGCTGCTGTCTGGAGTTCAAGTGCAGTGGGATGCTCTATGA
 TCAGGACCTGTGGACCGCACCTTGGTGAAGGTGATCCGCCAGGCGAGCTCGGCTCGAGGCGATGTGAACCCA
 TGCTCGATGAGTACCTTGTGCAACCACTTGCCACTTGCAGTCAACACGACACCACTGAGTACACCATGCTGGCA
 CCGCTTGGACCACTGGGCAACCACTATGGCATGTACACTGTGCTGACGAGGACCTGCGACGCGCCAGAGAT
 CGGCTCGGCGCTGCTGTGATGCGACATCCGATGCTCTCCAGAAATCATGAAGAGCATGTGGGAGTGGCC
 TCACCTTCAACTCTGTGAGAGAGCAAGTAGGCGCGAGAGTGCTTCCAGTACTCCAAAGCACCCCGCCGAG
 TCCCTTGTGTCGAGGCACTGCTCAAGGAAGAGTGCTGCTGAGGAGGCGACAGGCGAGGAGGCTGGCGAGG
 CCAGGTTGGAGTGGTGCTCTGAGATTCTAGATGTTGCTCAACAGCCCGCTGATCAAC**TAA**TTTTTGTGGT
 ACTTCACCTCTTCTGCTGCTCATTTGATGTGACAGCATTGTGAGACTGACCAAACTGCACTGGTGAAT
 TTAGACTCTGCTTCTGATTTGCTTGTGTTCTTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCT
 TTGGCACTGGCCGCCACATGACATTAAGGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 TGCCACTGGTAAACTCTGAGCTTCAACTGTACTTCTTAACTGAATTAATGCAAAATGACTTCTCTCTTCT
 TTGTGATGGTTTGGCCACTCTGCAATAGTGATAATCTGATGCTGAGATCAATAACCAATGATAAAGCATAT
 TTCTTGGCTTGTCTCCACAGGACATAGGCAAGCTTGTATCATAGTTATACATATAAATGGTGGTGAATAAAG
 AAATAAACACATACTTTTACTTGAATGTAATAACTATTTATTTCTTGTGTAATTTGGAATTTCTAGTGG
 ACATTAAGATTAAGCTATTAATATAAGGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 TCCACATATACAGGCTTCTGATCTGTATTTGTACATTTCCCTTGCATTCGCTTTGTTCTCTGTAGAAAC
 CCAGTGTAGCCAGGCGAGATGTCAATAATGCACTCTGTATTTCCGAAAAA

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FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTGGTTTTGGGATCTGCTTTGAGGTCCCATCTCTCATTTAAAAAAAATACAGAG
 ACCTCAATACCCGTACGCATACATACATATGTGTATATATATGTAACCTAGACAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAGAATTTAGAGATGATTATTGTCAAGATCCCTGTGGATTGATG
 CCCTTTGGGTAGCGTCTCCTCAGTGATCGAGCCCTACCCCTTGGTTGGGGACATTTATGATTTGTGTAAGACT
 CAGATTTACACGGAAGAGGGAAGTTTGGGATTACATGGCTGCCAGCCGGAATCCACGGACATGACAAAAT
 TCTGAAGTGAAGTCTCGATCTCCGGATATTACCTGTGGAGACCTCTGAGACCTTCTGTGCAATGGGCATC
 CCTACATGTGCAATATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTTGAAGGAGTATCCCAAGCCCTCCAGSETTAACAT
 CACTCTGCTCTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATACAGCATACGGCTCTTAGAATCATTTGACACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATCCACTTTGAAATCAAAGACAGGTTCCGGCTTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCCTT
 ACAGTCAACAGACCTGAGGATAAGGCTGTTAAGACAGCCGTTGGGAAATATTTGTAGATGAGTCACTTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGTGCAGTGTAACTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGGACAACACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTTACAGGCGCGACTTGGAGTCCAGGCTCCTATCTCCCCATCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTGTTACGAATGTCTGCGACAACAGAGCTCCTGCACTGCCAGAACGGAGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCGCATACAGGGCATCTCTGCGAGAAGCTGCGGTGCGAGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCAGGGCGCGCCCCGCCACGGCACCCACGCGTGTCTGCTGCTGACACGCTGTCT
 GGGAAACCGCCAGCCCTGCTGTTCTAGGTTGTCACCTCCAGCCACACCGGACGGGCTGTGCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAATACATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTAACTGAACATAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT
 TGACTCCAGAGGAGTTGCGAGCTGTGTATATTATCACTGCAAAATCATTGCGAGCTGCAGAGCATATTGTGGA
 TTGGAAGAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAACAAATCAACCGACCTAAAAACATTGGC
 TACTCTAGCGTGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGAACCAACCAATAGCATTTCTTGTGTGTCAG
 GTGCATTGTGGCATAAGGAATCTGTTACAGCTGCCATATTGGCTGCTTCCGTCCTGAATCCCTCCAAC
 CTGTGCTTTAGTGAACGTGCTCTGTAAACCTCGTGGTTGAAAGATTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAAACAGCCCTCTAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACCCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGATCTATCCCTTTTGATTTCAATGAAGTT
 ATTTTTCTTGAACACTGTAATATGTAGATTTTTGTATTATTGCCAATTTGTGTACACAGCAATCTGTTAAT
 GTATCAATTCGAATCAGCAAAAGACTGACATTTTATTTGTCTCTTTTCGTTCTGTTTGTTCACCTGGGACA
 GATTTCTCTGTAAGGCAACGAACGCTGCTGCATCAAGAATATCAGTTTACATATATACACAGTGTAAATAGA
 TTCCACCAAGGACATTTCAATGTTTTCTGTGTGTTTTAATCCTGGAAGATTAAAAAATAAACTCCCTGCA
 TAAACGATTTTCAGGAATTTGTATTGCAATTTCTTAAGATGAAGGAACGCCACCAAGCAATTTCACTACCT
 TACTGATTTCTGTGGACTGAGTACATTCAGCTGACAAATTTAGTTCGAGGAAGTGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTCCACTTGGGAAAAATTACAACAGCAAAAAAATAAAAAA
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FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVVDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDGCKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

CCACACGCTCCGGGTGACCTGGGCCGAGCCCTCCCGTCCGGCTAAGATTGCTGAGGAGCGCG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGCTCCGGGCGAGGTGTCTCATGACTT
CTCTTGTGGACCA**ATG**TCCGTGATCTTTTTTGCTGCGTGGTACGGGTAAAGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTCTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCTCGAGACCCCTGTGGTGGGAATTCACAGCTTCCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGACGCTTGGAAAAAT
TCAGGAGGAGCTCAAGTTCAGCCTCCAGCGGTTCCTACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTACACACCGATGCACCTTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
CATTGAGGAGTTTCACTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAATCTCATCAGCAGGAGCCTGTGGA
AAAGGCATGTGAGTGAAATCTGGGAATGGCTGGATTCCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCAGGATTCTATTTGT
TTAATGGGCTTTTCTACTAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTCAATACTTGCTGTTCATGTTACACAAGCTTCTTACGGTTTTTC
TTGTAACAATAAAATTTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC
TAAACTTGATATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAAATTAATG
AAGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTTAAAAA
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FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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CTCAGCGCGCTTCCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAACGTGAGCGCA
CCGACCTTTAAAGAGCTGGGGAGCAAGGGAGGACAGAGCCCTTTAAACAGCGAGCGGGTGCTG
CCTGCCCTTTAAGGCGGGGCTGCCGAGCACTGTATCTAGGCCCCAGACTGCCCCAGTT
TCTGTGCGAGGCTGCGAGGAAAGGCCCTTAGGCTGGGTCTGGGTGCTTGGCGGGCGGCTT
CCTCCCGCTCGCTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCTGTCGACGAGTA
TGGAGAGCACTGTACTAGCAAGTGCATTCGCTGCGAGAACAGCTATTCCACAGAGGATCCGC
GAGTGATTATATCAACACTTCTGTTTGCAACACTGTACATCTCTGCGCAACTCTTCTGGA
CCGCTTTCAAGAAGCCTGCTGAGTTACCACAGCTGGATGATGAAGTCCACACCTCAACAAGA
TTGGCTCGAGCTGTGACCTTTACCTTGCAATTGCCCTGGGTGCTGCTGCTGCTCGCTGCC
TTCTCCATCATCAGCAATGAGGTGCTGCTTCCCTGCTCGGAACACTACATCATCAGTGGCT
CAACGGCTCCCTCATCTAGCTGGCTCTGGAACCTTGTTTCTCTCTCCCAACCTGTTCCTCA
TCTTCTCATGCCCTTTGCATATTTCTTACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
GGTGCTCTGGGCGGGGTCTATGAGACAGTGGTGAATGTGATGCTCCCACTCTGCTGGTGCT
AGGATGGTGTGGTGGCATCAGCACTGTGGACAAGAACAGGCCAACAGAGATGACTCT
ATGACTTTTGGGAGTACTACTTCCCTACCTCTACTCATGCACTCTCTCTTGGGGTCTG
CTGCTCTGGTGTGTAACCTACTGGGTCTCGGCCGCACTGTTCTCCGCTCACTGGGAAGCTGCT
AGTCAAGCCCGGCTGCTGGAAGACTGGAGGACAGCTGTAAGTCTGACGCTTTGAGGAG
CAGCCCTGACCCCGAGATCTGTAATCTTCTACTCTCTGCTGCTGCTTTAGACATGGAGCTG
CTACACAGACAGTCTGGCTCTGCGACACAGAGGGTCTGCTGGAGAAGAGGCCGAGGCT
TTCAGCTTGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGCTGGTGTGCTGACGG
GCCCTGTGCTGCTATTGTGGCCATCCACATCTCTGGAGCTGCTCATGATGAGGCTGCCAT
CCCGGAGGACTCGAGGTACTCCTTAGGCCAGTCTCCTCTTCCAAGCTGGGCTCCTTTGG
TGCGTCACTCAGTGTGACTCATCTTTTACCTAATGGTGTCTCTCAGTTGTGGGCTCTATA
GCTCTTCACTTTCCGAGGCTCGGGCCAGATGGCACGACACTGCCATGACGCAGATAATT
GGGAATCTGTGCTGCTGCTGCTGCTTAAGCTCAGCACTTCTGTCTTCTCTGCAACCTGGG
GCTCACTCGCTTTGACTGCTGGGTGACTTTGGAGCCTTCAACTGCTGGGCAATTTCTACA
TTGTGTTCTCTACAAAGCAGCCTTTGAGCCTCACCACACTGTGCTGGTGAAGCACTTCT
ACTGCAAGCTGTGCGGGCAGAGCTGCTCGGGGCTTTGGGCTGGACAGACTGCCGTGCCGT
CTCCGGTTTCCCCAGGCATCTAGGAAAGACCCAGACCAAG**TGA**CACTCCAGCTGGGGTGGGA
AGGAAAAAATGACATGCACTGCTGCTGCTAGGCCCTGGAGGGAAGCCCAAGGCTACTTTGG
ACCTCAGSACCTGGAATCTGAGAGGTTGGGTGGCAGAGGGGAGCAGGCCATCTGCATATT
GCATAAATCTGAGCCAGAGTTTGGGACCGAGCACTCTGCTTTCCATACTTAAGTGTGGCT
CAGCATGGGTAAGGCTGGGTGACTGGGTAGGCCCTGATCCCAATCTGTTTACATCA
ATCTGCTCACTGCTGTCTGCGGCATCCCCATAGCCATGTTTACATGATTGTATGTGCAAT
AGGTTGGGTAGGGCAGGAAAGGACTGGGCCAGGCGAGGCTGGGAGATAGATTGCTCTTC
CTTGCTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCTGGAGGGGCTTTGGACCACTG
AAAGACCAAGGGGATAGGGAGGAGGAGGCTTACGCACTCAGCAATAAAGTTGATCCAGGGA
AAAAA

FIGURE 79

MEAPDYEVLVSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVVK
IALELCTFTLAIALGAVLLLPSIIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGGAVIQVVLI FYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDGFRFNWLGNFY
IVFLYNAAFAGLTTLCVLKFTTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGNITCNTCCCC
GCTCGTCCTCCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGCTCCGGACGACTGTATCTGAGCCCAGACTGCCCCGAGTTT
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGCGCGCGGCGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTGGCAATTGCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
 GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**ATG**CTGCTGT
 GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGCAAGGACCCAGGCCCAT
 ATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGTGAACCTCAC'TGCAA
 GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
 TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
 GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
 TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
 AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTGAAGGAGAC
 TCTGTGGTTCTGAGGTGCCGGGCAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
 TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
 AAA

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGPFAAQAANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCCTCACAGGGCCGGGTGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTGTGCTGTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTTAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCCGACCGGAACCCCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTTAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAGTAGTGAATGAAGAACAAGCGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 GTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCAACTTTGACAACAACAATATCAAGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTGCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNI PRGSDI IVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVVCDECPNVKL VNEERTLEVEIEPGVRDGM EYPFIFEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHK VHI SRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGTNGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCANTTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCCTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCGTGATGATCCACAAGCCCG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAAGTGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGGCGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGAGCC
 TTGGTGCTGGTTTGACAGGCAGCGCTACTGCGGCGCGGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTCACTCTGAC
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAG**TGCCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCGGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACCTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG
 TGTGGCAATTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAT
 ACAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAAACAGGA
 TTTGGAGTGTTTTCTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
 GGGCTTCTTCTCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TAA**CAACA
 AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

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GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCGGCTTCATTTCTCCGACTCAGCTTCCC
ACCNTGGGCTTTCGAGGTGCTTTCGCCGTGTCCCCACCACGAGCCATGATCTCCTTAA
CGGACACGCAGAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTAGATTCCTCTTCCAAAACATAAAATGAAG
CTACAGGTTTTTTCTGGGTGGTGTATTGATTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGAGTTTTTCTCTGTGTC

GGGACACGAGGCTGAACCCACGCGGCTCCATCTAGCTTCTGGTTTCTAAGTCATGTGCCAAAT
GGCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTTGGATCTTTCTCTCTTCTGGAATCTTTGA
CTGTGGGTAGTTATTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTACGCTCTTCACTCTCCTCCTCTGGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGTCTGAGGATGGTGGT
GGGGCACGGAATGCACCATCTTACGAGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTCCT
GATTCACTGTGAGGCGACCGTTTACCGAGAAGAGCATGAGATCAGCATGAGCTGGCGCC
GGGCGAAGGGGCTCCCTCGCCTCAAGCATACCTTTGTGCCACGAACCAAGGGCTTCGCCATC
ACCGTAGAGAGCTTGAGAAATGTAGTTTCAAGTGTATATGACTGTACACTCAATTTAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAGAGAATACCATGCAGATTTGTATG
TTAGGAGGATCCCCTGGAAGACATCCCTGAAGACGATGACGAGTGTCTGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCGAGA
GACGCCCATGGTGCCCCCGCGCGCCCTGGACCTCTGTGAAGTGGTGTGTTTGGGCTTCG
TGGTGTCTTACCCTTTCTTCCAGTTCTGGTTCAGCATGATCAGGAGCGGGTCTTCCCTACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGCGGGAAGTACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTGTAAATCTTT
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGACCGAAGGGGACAAAGTTCCTTTCATCTTTTGGTGTGAGTGTTCGT
AACCTCTGGTTGCCAGACATAAGATGAAAGTGCTTTTAGTGAGATGACTAAATTTATGCCTC
CAAGAAAAAATAATTAAGTGGCTTTTCTGGGTCAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIAAGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYKENAIVVLNHNKFEIDFLCGWSLSEFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSRLRNVVSAVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVWRWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACACTGGGTATATAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAAGTGGAAAGACAGTGAACAAGCAGTAGATAAAT
 AGTAAAGGATGTAACAGATTAACACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATCTGAATTTCTTCATTCATGTGTTATGTCTTAAAAAATAGACA
 TGTCTTAAAAAGTAGCTGTAACACAAACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCCTTTTAAACCTTACAAGGAGATTTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTTCATTGTTTTTACTATGTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTTCTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATTGCTATTAAAAATAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNTSDSTEGFLLGEVKGAEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITFESCSTHRLHSLYKPGKGLFHRVPLVANLGMSEQLGKYTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQDKPQENIFLCIQALRLFTFFPNSEFLHSCVMSLKNRHVSKSS
CINNYHLDVVDNLTLMVETHDIPEASFASNTFQIKHALDLDDRWFQKRSRLDTPDKRSKA
NTGSSNODKASKMSSPTEETEEKMGFGYRSRPTF

GSCACAGCGCGCGCGCGGAGGCGCAGAGTCAGCGCAGCGTAGTCCAGCGCGGACGAGCGGACAGCGCGGAGCAG
 CCAGGACGAGCGCGGAGCGAAAGCGCCGCGCGCGCCGACACACTCTCGCGTCCCGGCGCGCTGCCACCTTCCT
 CTTCTCCCGCGGCTCCCGCGCTCGCGCGCAGCTCAGTCTGCGCGGCTTCGCTGCCCGCGAAACCCGAGGCTCACC
 CGCCGCGCGCTCTGCTTCCCTGGGCGCGCGCGCGCTCCACGCGCTCTCTTCTCCGCTGGCGCGCGCTGCGAC
 GGGGACGGCTTGCCTGAGCGGCGCGCAGCTACTTCTTTCGCCCGCGCTCTCTCCGCTTCTCGCTCTCTCCAC
 CAACCTCAAATCTCTTCTCCCTACAGCTCGGAGCTCGTAGTCCCGGACTCCGCGAGCCCTCGCGCGGCTCGCGTA
 CGCGCTCTCCGCTCCGCTCCCGAGGTCGGAAGCGCTCGCCCGCGCGCGACATGCGACGGTTCGGCTTGC
 CGCGCTTCTCTGCACCTCGGAGCTCTGCTCAGCGCGCGCTTGTGCTCGCGAGTCAAGTCAAAAAGTGTCTCGG
 AAGTCGACGCTTTCTTACGTTGTCCAAAGCTTCAACAAAGACATGCCCTCCAGAGCAACAGCTGATCGCT
 TTAAGAGCTCTGCCCGAGGCTTCACTCTGTCTCTCAGAGATGGAGGAGATGACGCTCGAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGGCAAGACTGCAATCATTGGAAGCTGCTTTGCTTCAGTTCAGTCAAGAAAGTTG
 ATGAATTTCTCAAAGATCTGATTTGAAATCGAGAGAAATCCGTAAGTATGTTTGTGAGACATATGGCCAT
 TTATACATCAAAATTTGAGTATTTAAAGACTCTCTTGAGTGTGAAAGCTACTAGCTGTGTGGGAATGT
 GAACCTGGGAAGAAATCTGAATGACTTTGGGGTCGCTCTCTGGAGCGGATGTTCGCGTGGTGAATCCCGAT
 ACCAATTTACAGATGAGTATTTGGAATGTTGTGAGCAAGTATACGGGACAGCTGAAGCGCTTCGAGATGTCTCC
 CGAAATTAAGCTTCAGGTTACTCTGCTGCTTTGTAGCAAGCCGCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCGTCGACCAAGTCTCTCGTGGTAACCCCAAGCCGCTGTACCATGCCCTGTGAAGATGATCTACT
 CTTCCCACTGCGCGGGTCTCGTGACTGTGAAGCACTGTACCACTACTGCTCAAACTCATGAGAGGCTGTG
 GCGCAACCAAGGGATTCGATTTTGAATGAAACAATTTCAATAGTCTATGCTGTGTTGAGAGAGGCTAGA
 GGGCTCTTTCAACATTTGAATCGGTCAATGGATCCCATCGATGTGAAGATTTCTGATGCTATTGAATCAAGG
 ATAAATGTTGTCAGTGTCTCAGAAGTTTCCAGGATGTGGCTCAGGAAACCGCAATGAGATGACTGTTGAATGG
 AAGGCAAGGACAGGTAAGCTGTTTCGATGACAGGAAATGGATTGCGCAACCGGGCAGCAACCAAGGCTCG
 GGTGTACACCAAGCAACAGCATCACTGATCCTTGTGCAATATGCTCTTCAGTGTGACCAAGCAAGATGA
 AGAATAGCTACATCAATGGGAACGCGTGGAATCTTTTGATATCAGTGAAGAAATAGTGGAGAGGAAGTGGAAAGT
 GCGCTGTGATTCACAGACGCGCTTCAGATTTGACTACATGCGCACTGACATGCTGGGAAGGTGCCATGA
 GAAAGCCAGCAGCTGGTGGTTCGCTCTGGGGCAGCGGCTACCTCTTCATCTGTCTTCGATCTTTCTTCGCTG
 TTATGACAGAGAGTGGAGTAAATTTCAACTCTCAGGAAAGTGTTCATCAAAAAGTAAAGGCGACAGGTT
 ATCACTTTTCAACATCTAGTGAATTTGCTTTTAAATGAATGAGCAACAATGTACAGTTTCTTACTATGTGGC
 CACTGTGTTAAAGAGTGTCACTTTGTTTCTTCATCAGTTTGGGAGGAAAGGCACTGTGATTTAGTGTGAGT
 TCTGCTGCTCCCAACCAATGCTTAAAGCGTGGCTACAGTGTAGGTACAGACATATAGTTAGTTGTGATTTGTGA
 TTTTATCACTCTATTATTTGTTTGTATGTTTTTCTTCATTTCTGTTTGGGTTTTTTTTTCAACTGTGATCT
 CGCTTGTGTTTCTCAAGCAAAACCGGGTCCCTCTTCGCACTGAATCTAGTATTTCTGAAATATTAATA
 CGTGTGACAGGACGGTTTTATTATTCATGTATCTTCTTTAAAGAAAGGCGCCAAAAGG

MARFGLPALCTLAVLSAALLAELKSKSCSEVRRLVYSGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKSVVNPTAQCTHAL
LKMIYCSHRCGLVTVKPCYNYSNIMRGCLANQGDLDFFWNNFIDAMLMVAERLEGFPNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGCPPKPLPAGRISRISISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPNSVCNDERMAAGNGNEDDCWNGKGKSRYL
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNNGNDVDFDISDESSGE
GSGSGCEYQOCPEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCTGAGAGCCCCAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
 AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
 TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
 GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
 CCTAAATCATTCAGTGCTCTCAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGCTCTC
 TCTAGTGCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGC
 AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

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AATGGCTGTCTTAGTACTTCGCGTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCTTAAGCCTCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGAATCATCTCAGGACACACCCATGTGGCTCTGGACAATCCAAGAGCA
GCCAAATCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCAACAGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRLTVVLGLLVLFILTCYADDPKPKDDSGKDPKPDFPKFLSLLGTEIIEHAVE
FILRMSRSTGFMEFDDNEGKHSSK

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GGACGCCAGCGCCTCTGACAGAGGCTGAGCAGGGAAGGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCTGACGCTGCTGGTCTGCTTCTTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGAAAGTGCCCTACTGGAGCTGG
CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCCTAGACC
CAAATCCCCTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTGTGTCAGAGCCCAAGGAAGTCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCTATGTGGCAGCAAGTTTTCTGAGCCACCTGGAAACATATGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTCTCCGAAATCCAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAGGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCAACGTTTGCTTCCCAATGTTGTC
CCTTCTCCTCGTTCCCATGGTAAAGTCTCTCTCGCTTTCCTCCTGAGGCTACACCCATCGCT
CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAACCCCTGACCCCTCT
CTCCCCACTAACACCTTCTTCTGAGTGGGGGACCAAGGGGAATCAGAGATGCTGGGGAT
GCCAGACAGCAACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTTTAATAAATAGACGA
AACCAGC

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGGGTGANFQFYPPGCRVTCIDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDDVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEFPGSWAFM
WQQVFEPWTKHIGDGCCLTRETWKDLNAQFSEIQMERQPPPLKWLPGVPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPRLGT

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FIGURE 104

GTGGGATTTATTTGAGTGCAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCAATTCGTAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCCTCCGGTCTGGCTCAACAG
 TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCACGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAATGGAACGACAGAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
 AAGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTCAGCTAGGTAAGATGACAAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTGAGCTAGCTGGTACAGA
 TAATTCAAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAAACTT
 ACATTTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDR LGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQG DILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNI TNQLEKWMKLNVEEGLYSRTLAGSITTPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCTCGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGCTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACTTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCCGACGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACAGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGTTATATCCA
 GACCCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAACATAAAGTGAAA
 CAGAATTTGAAGTGAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAGAAAGATGTGTCAGCTAG
 GTAAAGATGACAAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAAGAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAATCAAACTGCTGTGGTTTTAATTTT
 GTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTCAATAGGTAAAAA

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FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCTATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCGCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPSPLEPRT

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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCTCTCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTGCATCTGTTTTGATAATGATGTTGACACCCCTCCACGAATTCCTAAGTGGA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCCTCTGTTTCACATTTTCATTTTCATTTGGTTAT
 TTTGGGATFTGTTGTTGTCGCGGTGTTTTATGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTTGGACACAGAAAGGGAAAAATATGAAGTGCCTGTCTGGGTTTGCATCGTA
 TCCACAGGCATCACGGCAGTGTCTGCTCGTCTTGATTTTTTGTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAATCACAATAAAGCCATCAGCAGTGTCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACTCGAGGAGCTGCGCCAGGTTATGGAAGCGGCCAAGTGGAAATAGAAGCCCT
 TCTGGCGATTCGTGACATGTGTCCTGACCATTTAATTTGGCCTCATCTGGACATAGTGAATFCA
 TTCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTATTATTCAACAGAAGT
 AAAAAATGATCCTCCTGATCATCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGTCATTTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTTGCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAACTGCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCAATCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTTGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTTAAACAATGCAAGGCCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGAGGGGAACAGAACTCCAGGCATTGTGAGATAGATAGATACCCATTTTAGGTATCTGTACTCT
 GGAAACATTTTCTTCTAAGAGCCATTACAGAAATAGAAGATGAGACCCTAGAGAAAGTT
 AGTGAAATTTTTTTTAAAAAGCCATAATAACCCCTATTCTCTCCFAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
· YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCTT
 AGAATAATTTTGTATGGGATTTGTGATGCAGGAAAGCCCTAAGGGAAGAAAGAAATATTCATCTGTG
 TGTGGTGAAAATTTTTTGAAGAAAAAATTCCTTCTTCAAACAAGGGTGTCATTCTGTGATATT
TATGAGGACTTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGTCTGTG
 TGACTGGAGTACATTCAAACAAAGAAACGGCAAGAGATTTAAAGGCCCAAGTTCTACTGTG
 CCTCAGATTAACCTGGCATGTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGTAAT
 TCCAGCAGGATGCCAGACCCCAATACCATGTTTATGGCACTGACGTGTATGTCATCCCTACT
 CCAGTGTGTGGGGCTGGCGTACACAGTGGTGTGCTTGTATAATTCAAGGAGGGAATACTT
 GTTCGGGAAGGTTGCTGGACAGTCTGTTTACAAAGGGAGTTATTCACACGGTGTCCAATCGTT
 ATCCCTACACGATCGAGAGAAATCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGGTGTAA
 CCTACCATCAGCTCTTACATACTCATCTCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAAAGCCTATCAGAGAGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGTCTGTCACTGTAGCTGTGGCCACCCACCACTTGCCAAAGGCCATCCCCTTCTG
 TCTCTTCTACACAGCATCCCAGAGACCAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCACAGACTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGAGGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC
 TTGTTCCAAAAGAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTCTCGCTTTTTTAATTGATGGGAGCACCCAGCATTTGCCAAACGGCGCTCCG
 AATCCAGAAGCAGCTCTCGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGGTCCAC
 TGATGGGTGTTGTTCAGTATGGAGCAACCCCTGCTACTCACTTTAACTCAAGACACACAG
 AATTTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTCTAATGT
 AGGTCTGGGCTATCTCTTTGTGACCAAGAATCTCTTTTCCAAGCCAAATGGAACAGAGGCG
 GGGCTCCCACTGTGTGGTGGTGGATGGTGGCTGGCCACGGCAAAAGTGGAGGAGGCT
 TCAAGACTTCGAGAGAGTCAGGAATCAACATTTCTTTCATACCATTTGAAGGTGCTGCTGA
 AATGAGAAGCAGTATGTGTTGGAGCCCACTTTGCAACAAGGCCGTGTGCAAGCAAAAG
 GCTTCTACTCTCTCACGTGTCAGAGCTGGTTTGGCCTCCACAAGACCCCTGCAGGCTCTGGTG
 AAGCGGCTCTGCACACTGACCGCTGCGCTGACGACAAGACTGCTTGAACCTCGGCTGACAT
 TGGCTTCTGTCATCGACGGCTCCAGCAGTGTGGGGACGGGCACTTCGCGACCGTCTCCAGT
 TTGTGACAACTCACAAGAGTTTGAGATTTCGACACGGACACGGCGCATCGGGGCCGTG
 CAGTACACTAGCAACAGCGGCTGGAGTTTGGGTTTCGACAAGTACAGCAGCAGCCGTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCGACAGCAGGGGGCTGGCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAGTCCAAGCCCAACAGAGAGGAGTTAATGATCCTC
 ATACCGACGGGAGGTCCTACGACGAGCTCCGGATCCCAGCCATGGCTGCCCATCTCAAGGG
 AGTGAATCACTTATGCGATAGGCGTTGCTTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
 CTACCCCGCCAGAGACACTCTTCTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTTAACTCAAGCCTCGGAAC**TGA**ATTACAG
 CAGGCAGAGCACCAAGTGCCTTTACTTAACGTGACGTGTTGGACCACCCACCGCTTAA
 TGGGGCCGACCGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGCTTGTATTATTA
 TTCTTTGCGCATGCTTTTTTATATTCCAAAACCTTGGAGTTACAAGATGATACAAACGT
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGAACAAT
 GTTTTAAAAATAAATGTTGGAAATACAGTGCAGCCCTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTTATTTCTGATTTGAACCTCTGTAACCCCTCAGCAAGTTTCATTTT
 GTCATGACAATTGAGGAATTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAAATAAAAA
 AA
 AAAG

FIGURE 114

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGTT
 GCGCCAGGTCCCACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCTGAGAATGGCTGAGGAGGCGGCCGAAAACTCC
 TCCCAGCCTTTACAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAAC TACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCAGATCCTTGGAGGCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
 CTAGAACTCGGAAGAGATGCTGTGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCGGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCAACCAACTTCATCCACAACATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTACCCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTT
 AGACTCCTCATAACACTGGATAAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLLWVQMYKGTVSMPIVQSLEAYWPGLQSLIGDIDNAMRTFLNYTIVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

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FIGURE 116

AAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGAA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGTGCCACTGTTCTGTCTGGAAATGGGCCGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGCGCTGGAT
 CTCATTAGGTTTTGCGGAAGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACCTGTCTAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTTACACACTGGGT
 GGCTTGAGAGCCCCTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGTAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACCGGAGGATC
 CATGAACACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGTGTAAGTACAGAATTAGCAATAAAAAGGGCCACCTTGGCCAAAAGCGGTAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPE
TVYYSVEYQGEYESLYTSHIWIPSSWCSTEGPECVDVTDITATVPYNLVRATLGSQTS
SILKHPFNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPVLALFAFVGFMILV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

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FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTGGAAAGAAAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCCTTGTCGCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGCGCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**CAT**GTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAAGTTTGGCCAAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGGCCATCCTGCCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCAACTGTGTGCTGAGTGGAGGAGGTGAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTAT**TAA**CCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTGCCAACAAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
 AAAAAGTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTTCATTGTAACAATCCA
 AACAAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRIYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKEPTWNFWKYLVPDVGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCGAGGGCAAAGCGAGCCATGGCTGTCTACGTCGGGATGC
 TGCGCCCTGGGGAGGCTGTGCGCGGGAGCTCGGGGGTGTCTGGGGGCCGGGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAAGGTTGTCGCTTCCTCAGTTCCAGAGAGGTTGGATCG
 CATGGTCTCCACGCCATCGGAGGCCCTCAGCTACGTTTCAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTTGGACAA
 AGCTGCTTCTGGCCCTCCTGAGCATTGGCCCTCTGCAAAAGGTGACCCGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTCTGGT
 TCTGTGAACCCAGCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGTGGGCTGCAA
 GGCCCTTGTGTTCCCAAGCAATTCAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTGTCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCTTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACCCAGCCAGACTTCTCCAGTTATGACATCTCGACCATTGTGTGGAG
 GTGTCAATTGCTGGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCAAGAGAACAGTCCCGTGACATTGCGCACTT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCCAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGGCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTCAGGTTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTGCATTGCGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACAT
 GTGTTTGTCAAAAACACCCCTCACCATTTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTGTGAATAAAGCAGCAGGCCTGTCTGGCCGGTGGCCT
 GACTCTCTCCTGTGAGAATTGCAACCTGGCTTTATGCACCTAGATGTCCCAGCAGCCAGGTTT
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAATGAAGAGCTCTGGATGGGT
 CGGGAACCTCGCTTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCTGT
 TCCATCCCCCATTTCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

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FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GGTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFQQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRPLDLTTVISVDAPLPGLTLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTGS PKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVAYGTTENS PVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCCKIVGRSKDMIIRGENIYPAELEDDFFHTHPKVQEVQVVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGGG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGGCGGGTTCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCGGTCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGTCTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACCTGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGCTGCCCTC
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACCTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGTCTGCGCTGGTTTGGCGCTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCTGGACTTTGGAGCGTGG
 GGTGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCACTCCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPPLVRLPPEPTT
VASTTSVTTTSTAPVRPTSTTKMPAPTSQTPRQGVHEASRDEEPRLTGGAAGHQDRNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGTCTGGTCTTCTCTGTCAGCCTGCTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCCCTTTTCATTATGATTACCAGACCCCTGAGGATTGGGGGACTGGTGTT
CGCTGTGGTCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGGCCCCAGGAGATGAGGAAGCCCAAGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCTGATGCT**TAA**GA AAAACCGCCACTTC
AGCAACAGCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCTCTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCCTTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTGTTAGTGAACCTGTGGACCTCGCTT
CCCAGGCAGGGGCTGAGCCATGTGCCATCTGCTCCTCCCTGCCCGTGGCCCTCCGATCAC
CTTCTGCTCTCCTAGGAGCGTCTTGTGTGCCGAGACGAGCCCTCCCTGATTATGGGATGC
GTAGGGTAAGAGCAGCGGCAGTGGTCTTCAGTCTGCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTCTATCATTTCTTCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCTTATCCC
ACCTGATCCACAGCTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAACC
CAGCGTTGACGTGAGGCAGGCTATGCCCTTCCGTGGTTAATTCTTCCCAGGGGCTTCCAG
AGGAGTCCCCTATCTGCCCGCCCCCTTACAGAGCGCCCGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCTGGGGAATGTGTCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCTTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG
ATGAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTCTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCCGTGGTCAG
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG
GTGTAAGGTCATAACGAGAGTGGGAACCTCAACCCAGATCCCGCCCTCTCTGTCCTGTGTT
CCCGGCGAAACCAACCAACCGCTGCGCTGTGACCCATTGCTGTCTCTGTATCGTGATCTAT
CCTCAACAACAACAGAAAAAGGAATAAAATATCCTTTGTTTCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTREVQPSGGSLWNLRRLLEPLDANVDA

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AAACTTGACGCCATGAGATCCCGGTCTTCTCGCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCTGGGTGGTCTCTGAGGAAGAAAGCACCAATTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTCTCTGAAATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAATGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GCAACATGCTCCACTGGAAGAGGGGGCTAGCGTGAGCGTGATTCTCAACCTACCATAACT
CTTTCTGACCTCAGGAATCAATAAAACATTTTCAATCAA

CAGTTCCTGAAATCAATGGAGTTAATTTTAGGGAATACAAACGACCCATGCGGGGTGGAGATTGC
CTTTGCCCTCAGTGATTCTCACCTGCCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACGTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTATATACTAGATGGCTTCCATTTACCCACCACTATTTTAAAGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAAGTCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCACCTATTAATTTGTAACGATTAAAAAAGAATAAGAGCAGCGAGACCTCTAGGAGAATATTT
TACTCCTGGGTGCCCTTGACACATTATGTAGTGAATCCCAAAATGTGATGTTAATTTAA
TGTTATTCATATATAGTACATTTCAGTTGTGATGTAATGAATAACCAAGATGATTTTCTT
AAAAGTTTGGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGCTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAGAAGGATCTAAGTCTCTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTAAATGGATGGAGCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCAGT
 GCCATGGAAAAAGAAAACCTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATCTCTGTCTCGGAAAAACCAAAACTTGTGTATGCGAATACACCAAAAC
 CAGGCCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGCCATCTTGT
 GGATCACTGCAATACAAGTATCTGTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGTCAAGAGATTGCTGAAAGGGGAA
 CCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATCTCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATAT
 TCCCAAAATGTTGAAAACCTGAAGT**AG**AGTATCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTAATCAAGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGATTTCTCTTTTGTAAAACCAATAAATCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAA

FIGURE 133

MEWWASSPLRLWLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYPCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

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CACCCCTCCATTCTCGCCATGCGCCCTGCACCTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
TCATCCTGGCCTTTGGCACC GGAGTGGAGTTCTGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
ACAGCCTCATGGCAGCTGAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCACTGGGTGCGCG
TCCTTGCTTTGTGCTCATGTTCATCTCCTGGCTCCTCATCTTAGCATCCTTCTCGTCTTT
GACTATGCTGAGCTCATGGGGCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
TTCCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATCTGAGTTTCAGCCA
CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCATGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
CTGACCACTCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGTCCCCTTCTGCACCGT
GGCTTCCACTCAAGAAGGTGGACAGGGTCTGAAGTTCAACCGCTCATAGCTGTCCCTCCA
GGCCCCAACCTTGCTCACTACCTCCGGCCCTAGCTCTGCACCTCCTTAGGCCCTGCCCTCT
GGGCTCAGACCCCACTGACTCAAGGGGATTCTCTGCTCTTAAGTCGATGACTTGGGGCTC
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTCTAAAAAAA

MAPALLLIPAAALSFILAFGTGVEFVRFTSLRPLLGGIPESGGFDARQGWLAALQDRSILAP
LAWDLGLLLLFEVQGHSLMAAEVRKAWTSRYFGVLQRSIYVACTALALQLVMRYWEPFKPGFV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPCVEVLLTVLWVVPTLGTDRLLLAFLTLTYLGLAHLGLDRQLRYLRAQLQR
KHLHLSRQPDGEAE

amino acids 1-13

amino acids 58-76, 99-113, 141-159, 203-222

amino acids 37-43, 42-48, 229-235

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
AGAAATTGCCAAACCATTGCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
TTTAATTAAGCATGGAATACAGAAAAACAACAAAACTTAAGCTTTAATTTTCATCTGGAATT
CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
TCAGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
AGCTGCTGTGGATGCGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC
CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
TCCCCACTACAATGTGATAGAACCGCTGAACTGGATGTACTTCTATGAGTATGAGCCGATTT
ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAACTGCTCTCATCAAAATCCATTT
CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
TTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTCTTAGAGGATGAACACCTTCTTTATGGT
GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAAACCATTATGGC
ATTCCAGTGGGTAACTGAGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACAGTAGTG
TTTTTCATAACTATGGCAATTTAGTGAAGTATCTTTTAAACCTTAACCACTCAGAGAAAGTTT
TTCACAGGTTATCCTCTAATTGATAATATTTCTTATAGAGGATTTTACCAAAAAACCCATAT
TTCTTACCAGGAGTATCCTTTCAAGTGTTCCCTCCATACTGCAGTGGGTGGGTATATATAA
TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCAACCATCAAGTTT
GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCATATCCAGAAGA
CACAAATCTTTCTTCTATATAGAATCCATTTGGATGTCTGTCACTGAGACGTGTGATTG
CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC
ACATGCCATTATTAACTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
GTGTTAAATAAAGTAGGTACTGTGAAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACTG
AACTGAAACTCATGAAAAACCGAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
AGGCCCTTCAAAGATGATATGTFGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA
GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACATGTAGAGTTTTATTATTG
AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
TGGTCATTATATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
CATCTTTATAGTCGAAACATTTTCCAGTTACTTAACTGATCAGTTTTATTATTGATACATCAC
TCCATTTACGTAAAGTCATAGGTCATTTATGCATATCAGTAATCTCTGGACTTTGTGTTAAAT
ATTTTACTGTGGTAATAATAGAGAAGAATTAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTD DTVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFP PYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTGGGATTATGGAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

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CAATTCTGAAACTAAICGTGTGCAGAATTGACTTTGAAGAACGATTGCTTTTTCAGAAAGTATA
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATTAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTCTGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAAGTCCAGCCCTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCG
ATCATCACCAAGAGAAGTAAAAGCTCAAGAGAAATCAACCAATCTCCATTAATGTGAAGCAG
TCAAAAAAGAACCTGAGGATGACACAGGCTTCCAAAGCCCTTACAATGGTGTGAAGAAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCAG
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGCCCTCGAAGACATCATAATCAT
GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCITT
GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGTTTTGCCTATCTACAGTGTGATGT
ATGGAICTCAATCAAAACATTAACAGCAAACCTGATTAGGATTGATTTCTTGAAACCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAAGTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT
ATACAGATAAAATCTGCAGACACTGTTCTATTAAAGTGGTTATTGTTTAAATGATGGTGAAT
ACTTTCTTAACACTGGTTTGTCTGCATGTGAAGATTTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTCTAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSRRSRSRSRSHSESPPRRHHNHGSPHLKAKHTRDDLKSSNRHGHRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKS KHHGGSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATATCGGGTCANAATTGNCTTTGAAAGCATTGCTTTTACAGAAATATAT
TANCTTTTGTAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCCTCGTGCCAAAGCTTGGCACGAGGGTGCACCGCTTCTCGCACGCGT**ATG**GC
GGTCCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCAGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCGGAGTACCACTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGGC
GGAGGAGACCTCGAGCTGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCCTCACCTTCCCAGGCCGCGGCTGGC
CCAGACCCACCGGAGCGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCCTGC
ACACCAGCTTCCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTCACGGGAC
TTCTTGACACAGCCGCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA
CTCTGGGCGCCTCTGCTGTGCTGGTGGTGTGCTGCTGCGGCTGGCGGTGACCCGCGCCCC
ACCTGCAGGCCATACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCGAGTACCTGACGCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGGGATTGCCGG
GGCCCTGGGTGGCTGCTTACTCCCCCTTCTCCTCCGTGGCGTCTTGGCTACCTCATCTGGT
GGACGGCTGCTGCCAGCTGCTGCCAGCCTTTTCGGCCTTACTTCCACCAGCACTTGGCA
GGCTC**TAG**CTGCCTGCAGACCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGGCGCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTCACCACAGTGCTGACCCGCGGCCCCCTTGGAGCCGAGTTTCTGCCTCA
GAACTGTCTCTCCTGGGCCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAGGAGCATGCC
GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLHLSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVVRVYCYVT
VVSQYLTPLILTLNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVVQQTAAARI
AGALGGLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS

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FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTATTAACTGGGCTT
 AATCTGAAGGTTGCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTGTAGCTGACAGAAGGTGGCCAGGGAGAAATGCAGCACACTGCTCGGAGAAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCTTGGCTCAGTCCCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCTGT
 TATTCAGAACCTGTGAAAGGTGCCCTCCACTACGGCTGACCAAAGATAGGAAGAGGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGAGCTGCCACCATCTCCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCTGCCTACGTGTCTCGGCAGAGGACGGGAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCCGAACCTAGGGCAGGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAAATAATCGAGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCGGACGAG
 GCAGGGAAAAATCTGAAAACACCCTGCCCCCTGAAGTCTTTCCAAGGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAAGTGAAGCCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTCAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGGCTCTCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAAGTTCCCGAGCAGGAACAATGGACAGGGCCCC
 GGATGCCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAA
 TAAAACCTGGTGCACAAGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAAGAAAG
 TGCGGCTCATCTGATTGAGGCCAGTGAAGACGTGTTCACTCTGCTGTGTCGCCAGGTTGCGGACGCGGAGCC
 CTGACATCTTTGAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACT
 CCCCAGCCCCCTCCATCTCAATACTTGTGTCATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGAGGGGGAGCATCATAGAGAATGGGATTGCTCTATCTATGTATCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTGTTGAATGTGGATGGGGTCGAACCTGACA
 GAGGTGAGCCGGAGTGAGGCAGTGGCATTTATGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTCGGCTCATGTGGCTGGAATTACACGGTGCTGTATAACTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCAATTGTAGGAGTTATGAAGAATCAATGGAAGAACAACCTTT
 TTTTCATCAATCCATTTGTTGAAGGAACACAGCATCAATGATGGAAGAATAGATGTGGTGATATCTCTCTTG
 CTGTCAATGTTAGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTTGGCTGGCACTTTTTCATAGAAATCAATGATGGTTCAGGAGGAACACAGAAAA
 TCACAATAAGCTAAGAAGTTGAACACTATATTTATCTTGTCACTTTTATATTTAAAGAAAGAAATCATTTG
 AAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAATATGATTCCAAAATAAATT
 AAACCTACTAGTTTTTTTTTCAAGTGTGAGGATTTCTCATTAATCTCAACACTGCTTATATTTTCTTCTTCAAT
 AAAAAGCCCTAAAACAACTAAAATGATTGATTTATATCCCACTCAATTCAGCTGATTTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCAAGGGTACATTATGGCCATTTTTAATTTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAAAGCTGTCTTTCATCAACCAAGAATAAATATTTTCAGAAGTTAA

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FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISFVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHQGLEENDRVLAINGHDRLYGSPESAHLIQASERRVHLVVSQRQVRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFPIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

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FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTT CAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATT CATGTTT TAGGATGATTAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACTCTCAAAGTCAAATTAAATCTTTCCCAATGCCCCAACTAATTTGAGATTC
AGTCAGAAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCCTTGCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAGCAGCAGCCATGTAGAATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTGGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPGKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCRPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPFPGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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GGTCTCTTA**AATG**CGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCTGT
CTGTCCGGCTGGTCCCAGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTGGGGAAGAAA
CTAAATGTCAACAGCGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTACAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCG
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTTCAGT
TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCACAAGATGAAAGAAAAGTGGGAGATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGGCTTGAGGACTTCTGATGGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCACCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCTT
TTGCCAACATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACCTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAATGATAT
GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGAATCTTTCCGTGTCCTGAAGAG
AATTTTAAATTTATTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
TGTTCTGTACTGATATTTTAAATAAGAGTTCTATTTCCAAAAAATAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRDPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

GGGAAAGCCATTTCGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTATATACCGTGGGAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTAAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTGTAATCAGAATTGTCTGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACCTCTCCCTTACCTTT
CCTCTCTCCATTCAAGCATCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCTATTTGAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGPTEQHFWARL

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TOSTT-TH0660

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTGCTCTA
 CCTCACGGCCGAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC
 AGAACTGCCCTCCGTTTGCTCGTGCAGTAACCAAGTTACGAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCCTGCAAT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGCCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTGCACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTGATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAT
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTCCTGTGGGTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCGCTGTGATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGAGCGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACCTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC
 TTTGAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGAGGCAACTCCAACGCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTCAAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCAGCTCCACTGGTTACACGCGGCATATACCACCTCTACCAGGTGCTCATTGAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACCTGACAAGATGCAGACCAGCCT
 GGATGAAGTCTATGAAGACCACCAAGATCATATTGGCTGCTTTTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGCTTCTATAAACTTCGTAAGCGGCACACGAGCGGGATACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGTGGACGAAGACATCCAGCAGAACATCCCG
 AGCAGCAACAGCAGCTCCGTCGGGTGTATCAGGTGAGGGGCGAGTGCTGCTGCCACAAATC
 ATGACCATATTAACATAACACACCTACAACACGACATGGGGCCCACTGGACAGAAAAACAGC
 CTGGGGAACCTCTCTGACCCCCACAGTCACCACTATCTCTGAACCTTATATAATTGAGACCCA
 TATGGAAGCAAGGTACAGGAACTCAATAT**TGA**CTCCCTCCCCAAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTTAAATTTAAAGA
 CAAAAGTCAAAACA

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FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYNLGMCNIKDMPNLTPLVGLEELEMMSGNHFP EIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSPHDLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGT LNF SHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LNTSNYSFFT VTVETTEISPEDTTRKYKVPPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLDEVMKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

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[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIEVCVPGKREVV
GYTIPCCRNEENECDSCLIHPCGTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHS DGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCE NLEERNCS DPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREP KISDLVRRRVLP MQVQSRETPLH
QLYSAAFSKQKLQSAPT KKPALPF GDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNLTLRSG
VVSVDLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCCACAAATTCGATTACTGTTGCTGTTGACTTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACCTACTTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCTCATTTTGGGGAAGGGAAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAATTGACAACCTGTCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCACTCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAACCCCTCAAGGAAGAAAAATGGGGAC
 TGCTTTTATATCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAATAACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
 AGACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCAGAGTGGATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAACCTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTTACAGCTCATTTGTTGAGCTGAATTTTCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTTGTAACAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGCTGTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACCTGTTATTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCACGAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGAGGGTGGAGTGTGCGCTGCAAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCCTATTAGTTTTTAAAGAGTTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
 TGCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNRREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEQKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWGWWGEGDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVVTAAADCWMCQPVARGF
VVLPITEFLVGD LVVTQNTSLPWSSYLTKTVLKVSVLLHDPNSFLKTALFLYSWDFGDTQ
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEVEPEPATRAVKQKTGDFSASIKLQETLRGIQVL
GPTLIQTFQKMTVTNLNLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIIISKTHQYHKIQVWPSRIQPAVFAFPCCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMC CGPFLETPSEYLEIVRENNHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTTGACAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCGTCCCCTCCCTTCCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCCTTTGTTTCCAAA
AAA

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

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FIGURE 166

CTGTGAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACCA**ATG**TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGGC
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACAGCTTTACAAGCCCTACACCAAC
 GGAATCATTTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTTGGGGATACCTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAAACAGACCAAGAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGGCCCTG
 CCCACACGTCTGGTTTGAAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCCAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCGT
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCCGCTCC**TGA**GCGCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGCTCTTCCAGACTCCAGGG
 CTCCTCCGGGCTGCTCTCGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTCACGCTGTGCGGGCTGAGTGGTGGGGAGATGTGGCCATGGTCTGTGTCTAGAGAT
 GCGGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCCTCAGGAAGGCACAGCTGAGGCACCTGCGCTGGCTTCGCGCTCAACATCCGCCCCAGC
 AATTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCTCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGCGGTTACTAAAGGGAGGGGAAGAGCCAGGTG
 GCGCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTACTCCAGGCTAACCCCTGAACCTCCCC
 ATGTGATGCGCGCTTGTGTAATGTGTGCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGAATCTTCAAGCTCACAGGCTGTTGTGGGGATTAAAGTGTGCTGCGGTTGAGTGA
 AGGACACATCACGTTTCAGTGTTCAGTACAGGCCCAAAACGGGGCAGGGCAGGCCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

MFLLLPFDLSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLIEEEIKIRRSKGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAEELESWNLLSRTNYNFQYISRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTVVGYLPNGRFKEEMSKHVHLMCYRICKVRALTAIITYHDRENRPNGGICVANH
TSPIDVILIASDGYAMVGQVHGGLMGVIQAMVKACPHVWFERSEVKDRHLVAKRLETHVQ
DKSKLPILIFPEGTCINNTSVMFMFKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVSKSVWVLLPMTREADEDAVQFANRVKSATARQGGLVDLLWDGGLKREKVKDTF
KEEOOLSLKSMIVGNHKDRSR

GCCCTCTGA^{AA}ACCAGGACTCCAGCACCTCTGTGCTCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGG^{ATG}CGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAG
ACCTGGCAGGCCCAGGCTGTTCCACCATCTGCCCTTGGGCTTGCTCCAGACACCTTTGA
CGATACTTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCACCATGCCCTGCTGCGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGGTTCAAAGCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAAGGCCGTGCATTCTACCTGATCCGG
GCCCTGCAGCTGTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGA^{ACCC}AAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTGGGGAGAAGAGGCGGGGCTGT
GTGTTCTGCCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCT^{TGA}AAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAATATGTTCCGGACCGGCACTTACGATCTCTCCCAACACGAG
ATGTTGGCTCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTTGCATGTGATGGGACTTCTCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGCTTTTATTGAGGTAGCT^{ACGT}GATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTL LLLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAAACCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCTGTGTCTCCTGTTGGTGGCCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

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FIGURE 171

MAGSPTCLTLIYLWQLTGAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFFDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTHEYDTIPHTNRITLKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGTCAGCAGCC
TCTGGACCCGTGAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCTCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTCCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTA CTGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA
ACTCCTAACATATGCCCCCATCTCGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
AGATGGAATCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

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GAAAGACGTGGTCTGTACAGACAGACAATCTATTCCCTACCAAAATGAAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCCTGTGACAAAAGA
GAAAAGATAGAAGACATGCAACTTTTAGACTTTTTCTGGAGCAAAATCCATGTCTTGGAGAA
TTCCTTAGTTCCTAAAGTCCATACTGTAAGAGATGAAGAGTGTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGTGCCTCCAGGCCGAGAATGAAGAAATGGCTGAGCCTCCAGTGTGTAGTGGAC
ACTTCTCAGGAGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTCCAGATTCATCCTCTGTCTACTGAGAAGTCCAAATGCTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATAACAAGACTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT
TTTTCATGAATTAATTCCTCTTCTGTTCAATAAATGATTACCCCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTAGGTCTATTGCT
TGTGTGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATMTSLTARKRACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL
IHFSVFLGLLL VGILEVL FGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGCTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAA**TAG**TGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCTC
GAACTGTGACATGGAGAGAGTGACCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTAGGCCCTTTCTGATCAGGAGGCTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPPLITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCCTGCC
 TGGCTGGGCCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTGTGGGCTC
 CTGGCTACTCGCCCGCATCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC
 AGTGTTTCCCACAGCCCCAAAACGGAACCTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCAACCAAGGATAATCTCTTCATCAGGTTCTGAAAGCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCTGGGATGCTGAC
 GCGCGCCTTCCATTTCAACATCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGAGAGAAAA
 GAAGCCAGCATATCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGCGCGCGC
 TTCCACAGGGCTGCCGCTGGTGCATGACTTTCACAGACGCTGTCTATCCGGAGCGCGCTCG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACTTGCAGGCCACCCAGAATACCAGGAGCGTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCTGACCATGTGCGTGAAGGAGAGCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTCGG
 CGTTGATGCTGCTGCACTTCCGGTCTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA
TGACTTTCTGACCCATCCACCTGTTTTTTTTGCAGATTGTGATGAATAAAGCGTGTGTCAAA

MSLLSLPWLGLRPVAMSPWLLLLLVGSGWLLARILAWTYAFYNNCRRLQCFQPQPKRNWFWG
HLGLITPTEEGLKDSQMSATYSQGFTVWLGPPIFFIVLCHPDTIRSI TNASAAIAPKDNLF
IRFLKPWLGEIGILSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLSAEGS
SRLDMFEHISLMTLDSLQKCFISFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFRHRACRLVHDFTDVAVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLSKDEDG
KALSDEDIRAEADTFMGGHDTTASGLSWVLYNLARHPEYQERCQREVQELLKDRDPKEIEW
DDLAQLPFLTMVCVESLRHPPAPFISRCTQDIVLPDGRVIPKIGITCLIDI GVHNNPTVW
PDPEYVDPRFDENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGT**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTCATTGTTACCTGGAATAAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLETGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

09990441-11501

FIGURE 185

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTT CAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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FIGURE 186

MPSPGTVCLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

090044.11604
T0911.140660

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLEYYVNPFPPTPGARVFVPRVRMCSGASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTTPRPAQGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGTG
 ATCACTCAGTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGAGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCTCTGCT
 ACTAACAGACTTGCTACTCAGTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTGCTG
 CTGTTTCTCTGTCTGTCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACACCTTCA
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCATAGTAAAGACTTCAAGGAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGAATTCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTS IHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSCQLGSRRLTTTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

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109111.1440660

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCCTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCCTATTCTCTCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCTGCCCCGCCGTAGATTACG
GACATTCGCCCCGTGTGTGCCACCAAACCAGGACTTCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

109177, 1440660

FIGURE 193

GTAGCGCGTCTTGGGCTCTCCGGCTGCCGCTGTGCCGCCGCCGCTCGGGTCTGTGGAGCCAGGAGCGACGTCA
 CCGCCATGGG CAGGCATCAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGATGTGCCCTTCCAAATATACAACAATACTGGCCCTCTTTGTTCTAATTTTTTACATCCTTTACCAATATCC
 ATACTGCATAGCAAGAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGAAGGAACITGCCATCTTTC
 TTACAACGGGCATTGTCTGTGACGCTTTTGGACTCCCTATTGTATTTGGCAGACACATCTGATTGAGTGGGGA
 GCTTGTGCACTTGTCTCACAGGAACACAGTCATCTTGCACATATACTAGGCTTTTCTTGGCTTTTGGAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAATTAAGTGAATCTGCTCAATGAGTCTGCTGACTTT
 GGTGGCCATTACGACACACAGGAGATGGGCGAGTTAATGCTGAATGGTATAGCAAGCCTCTTTGGGGTATTTTA
 GGTGCTCCCCTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGTCTGAAGGATTAAGGATTTTCT
 CTTTTGGAAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTTCTGTAGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAAATGTAATCA
 TTTGCATTGGTTAGGAATTAGAATTCGCGCGGCTATTTACTGGTCAAGTACATCTTTTCTCTTAAATTTATT
 TAGCCTCCATTATACAAAAAATTATAAAAAAAGTTTTTCACTGAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTTATACCTCAGAG
 GGGCCAAGTGTAAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTTATTTATGGAATGTCTACAGAGGAGTGTCTTTCTTCAATTGTTAGAAGAATTTATGTTAACTTTA
 AGGTAAGGGTGTAAAAACATTTTGTAGATAAGGTTTTTATTATGTTTATTATTTGTAGAGTGAGTGCAATGT
 GGGAGAAGATGACATTGAATTCAGTTTTTGAATCCTGTTTCTATTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTCACTGTTTTACCTGTTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGTATATATACATAAAA
 TAACCTTTTCAATATAGTTTAAATACACTTAGAAGTGTCTACTTACCTGGAAAATTAATGCTATGCCGTACAT
 CAGAGTGCCCTCCCTGCCAAGGCTTGGCATGATTAACAGTAACCTTGTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTAAGATTTAGACCATGGTAATAGTAGTCTTATTCTCTAAGGTTTATATCATATGTAATTTAAAG
 TATTTTAAGACAAGTTTCTGTATACCTCTGAACGTGTTTGATTTGAGTTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCAATTTGTTGTGAGTTAATGCAAGTAGGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAATTCAGCATACCAAGGCTGATCAATTTATAGTGGTCTTTTACATCTAATAATTTACAGGA
 CTTTTTTCAGGAGTGGGTTATAAAAACATTCAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG
 TTTATGAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTCACTTTTTTACTAAAGATGCCCTAA
 AGCCACAGSTTTTATGCTCAACTTAAGCCATGACTTTTATATGAGATGACGGGAAGCAGGACGAATATCG
 GCGTGTGGCTGGAGCCTTCCCACTGAGGCTGAAGTGGCTTGTGATTTATAATGTTCAAGTTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGACTGTGACAGACTTGGGAACCTTTTGTGCTGTGATCTACTGGACTTT
 TTTTTGCAAGGATGCAATCTCTGCTGCTTCCCTATTTTCTGTTCTGGATCTGACTGCACTGCACTGCTACTG
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCTATATTTCTATATACTAATTTGATTTGGCAGCAT
 GTGCTTTGACCTTTGTATAGTACTGCTTACATAGTGTCTGTCTGATTTCTAGGCTAGTTACTTGGATATGAAT
 TTTCCATAGAAATGACATGATACAACTTACCATTCTCTATGGAAGAAAACCTTTTGTATGATGAACAAATA
 AGATTTTAAATATCTATTTTAAAAAATAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

09090441.111501

[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCCLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKNFAHFPRLISLHSLCLRNRKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG
HLSAVTNRSIDLGPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGCGGACAAGATGG
TGTCACTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACAGGCACCTGGCCTCTTCTCGTGGACGCCGAGCGGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGGCGCGCTGA GCGTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPDGLV LASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRFTTRDEDLAVFLASR
AGRRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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[illegible]

TTGAGCGCAGGTGAGCTCTCGGGGTTCCGGGGGCGTTCCTCCAGTACACCTCCGGCCTTACCGCGGGCGCGC
CGAGGAGGTCTCTCCAGACGCTCCCTCCGTTGCTCCAAATATAGCGGATGAAGCGATCGCTCGCAGGCT
GGAGAGAAAATTTAGGGGAGAAAGCAGAGACACATACCATCATGACGATAGATTATCTTACACTG
AACTGATCAAGTACCTTTTGAAATAGCACTCGAAATTTATCTGGTGCTCTCATACTTGCCTGCACTGCTTCC
AACCCCTTTTCTCTCCAATAGCAGCAGCAAAAGGTTCTACTAGTTCTTTGATGGATTCGCTGGGATTA
TATATAAAGTTCCCAAGCCCCATTTCTTATTATATATAGTAAGAATTTGGTGTCTCAGCTGAAGCAGTACTAATGTG
TTTATTACAAAACCTACCCTAACCATTAATATTTGGTAATCTGCCTTTTCGAGAATCATGTGGATTTGTGC
AAGATGATTTGTTGTACTTCTTTCAGCAAAATCTTCTCCTTGATACATGAATATTA/TGATTCACAGTT/TT
GGAGAAGGCAGACCAATATGTGATCAAAACCGAGGGCAGACATATGTTGGTCAGCATGTGGCCCGGGA
ACAGATGTAAAAAATCATAGCGCTTTCTCTACTATTACATGCCTTACAAATGAGTCAGTTCA/TTCATGAAGATG
AGTTGCCAAATTTGTAATGGTTAGCTCAAAAGAGCAATCAATCTTGGTCTTCTCTATGGGAAGACCTG
ATGACATGGCCCAAGCTTTGGGACCTGACGTCGCGCTCATGGGCTGTCACTTCAGATATGACAAGAGTTA
CGATATCTCAACAATCTGCAAAAAGGCAGGTTGTGGAACACTCTGAACCTTAATCATACAAGTGA/CATG
AATGACGCACTGCTCTGAGGAAGAGTTTAATAGAACCTGACCACTCGGATGAAGACCACTAATCCCTGATG
ATCAATCTCCAGTCAGCGACTCTGCCAAAGGAAGTTAAATTTGATGAAGTCTTAAGAAGCACTAATCAGCT
CATCTTAATCTTACTGTTTACAAAAGAAGACCTTCGAGAAGGTGGCATACAAATACACAGCTGAATTC
ACCAATCATAGCAGTGGCTGATGAAGGTTGCACATTTACAGATAATGTCAGATGACTTTCTGTAGGCAACC
ACGGTACAGATATGCGTTAGCAGATATGCATCCAAATTTTGACCCATGGTCTGCCCTCAGAAAGATTTCT
TCAAAAGAGCACTGAACCTCCACAGATTTGTACCACACTATGACCCTCTCATATCTAGCTGCGACCA
CAATGATCATCTCGGAATGTCAGGATCGGCTCAATTCAGAAATGCCAGGTTGGTCCCTTATACAGAGTA
CTATACCTCCTCCTGGTAGTTGTAAACAGCAGAAATGACCAAGGGGTATCCCTTTATTCATAGGGGT
TCTCTTGGCAGCATTAATGATGTTGTATTTTGTAAATTTTCATTAAGCACTTTATTCAGCTCAATACCTGC
CTTACAAGATATGCACTCGAAATAGCTCAACCAATTTACAGCGCTAAAGCTTACTTTCAGCTGCATTTGCAT
TTGAAGTGGAGATTCOATATATATGTCAGTTGTTAAAGGTTCAAAATCTGGGAACCCAGTTCCAAACTCTG
AGAAACCAATTAAGAGCTATCATATTTAGGTATACACACACACACACACACATCATACACACACGCACTCA
ATACTACACCTGCAAGGAATAAAGATGTAGAGATATGTCCTATGTTCACTGTAGCATAGGATAGATAAG
ATCCTGCTTTATTTGGACTTGGCGCAGATTAATGATATATTTAGCAACTTTGCATATGTAAAGTACTTTAT
ATTGCATCTTAATTTTCTCTCTGCTGAGTGTACTTTAATTTGAATGCACTTTATGACAGTATATGTCTTAAC
TTGATTTGAAATGACAACTTTTTCGACCACTGTACAGAAATCTGTTACGATTTCTCAAATCGAAGGAATTT
TCTAAATATCCGGAATATGAACATAGAATCTATCTCATAAATGAGAGAGAAGAGGTGATAGTTGTGA
AAATTAATGTATAACCTTTGACCTTTGAATTTGGAGATGATTTCCACAGCAGATAGCACTGTGGGCTAT
TCTGTGCTTATTTCTTTCAGAGAAGCTGGTTTCTATTATTTTCCCTCAAAGAGAGTCAATACCTGACAG
ATTGCTTCTTAATATATGTTTCTGTGATAAAATATATGTTATTTCTGATGAGTCAATATAGTGTATTTCA
TAATATGAGACACCATGAATACATTTTCTTATATGTTGACGAATGGCTGAATAGAGCAACCGGCA
CCATCTCAGCAATGTTTCTCTGTGTAATATTTGCTCCTTTGAAATTAATATCACTATTAATTACATTA
AAATCAAATGTTTAAAAAAGAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNXSFSLDHMNIYDSKFWEETPIW
 ITNQRAHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPEKKGKDFEVEALHTAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPNGSFWNVQDLLNSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

GGATTTTTGTGATCCGCGATTTCGCTCCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCGAC
GACAGGCCACCTTCGCGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCCAACAGGGGACATGGCCACCTGGGACGAAAAGGCAGTACCCGCAGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
CTACCATGCTTGGAACTCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACCAGTCTCAGGGCAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
CCTGCCCCTGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTG
CAGCTCCCACAGTTTTCAGGTCATCATCATCTGCTGGTGGTCTGGATGCCCTCTGGTGC
TTGCTTGAGCTCATCTTGAGCATCAAGATCATTCGACCCGACAGAATAACTATGCTGCCATG
GTATPGACTACATGAGCATCACCACTCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
ATTTGTCTTCCGCTGAGTTCTTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
TGGTCTATTTCATCTTGACATTGTCTCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTACAGTGCTCTGAGAAGCCCTGGACTTGATGAGTTTGCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGATGGCATATGGGAATGAAGAAATCCGACTTCTACTCT
CACACAGCCACCGTGAAGTCTCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
TCACTTCAGATTACAATCACACAGAGCATCTGCCTGTTTTCAATCAACAAGAACAAAAAC
AAAACTATATAAGATATTCTGAAAAATTGACAGAAATTAAGACATAAAGCTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAGPAPRAPLDFRGMLRKLFSHRFQV I I ICLVVDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITLVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLILRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCGGCCAACAT
 GCTCTGTCTGTGCTGTACGCTGCCGCTCATCGGGGAAGCCAGACCGAGTTCCAGTATCTTGT
 AGTCGAAGGGGGCTCCTCGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCTCCACCTACCGCCAGTGGAAAGCAGAAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCAGCTAGACTTTGAGAATTTTGTCCATTTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTTTAAAGATTTTGGACAAAAAGAAATGATGGAGCCATGTACGCCGAGGAGATCATG
 CAGTCCCTGCGGGAGCTGGGAGTCAAGATATCTGAACAGCAGGCAAGAAAAATTTCTCAAGAG
 CATGGATAAAACCGCACGATGACCATCGACTGGAAAGAGTGGAGAGACTACCACCTCCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCCTCTACTGGAAAGCATTCCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGCAGACGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGATCCAGAAGCTGCACGGCCCTCTGG
 ACAGGCTCAAGGTGCTCATGCAAGTCCATGCCCTCCGACAGCAACATGGGCATCGTTGGT
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTGACCTGGCGGGGCAATGGCATCAA
 CGTCTCAAAATTTGCCCCGAATCAGCCATCAAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTTGGCA
 GGGGCCATCGCCAGAGCAGCATCTACCAATGGAGTCTGAAGACCCGGATGGCGCTGCG
 GAAGACAGGGCCAGTACTCAGGAATGCTGGACTGGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGCGCTCTACAAAGGCTATGTGCCCAACATCTGGGCATCATCCCTATCCCGGCATC
 GACCTTGCAGCTACGAGACGCTCAAGAATGCTGGCTGACAGCATATGCAGTGAACAGCGC
 GGACCCCGGGGTGTTTGTGCTCTGGCTGTGGCACCATGTCCAGTACCTGTGGCCAGGCTGG
 CCAGCTACCCCTCGCCCTAGTCCAGGACCCGATGACAGGCGCAAGCCTTATTTAGGCGGCT
 CCGAGGTGACCATGAGGACGCTCTTTCAACATATCTCCGCGACGAGGGGGCTCTGGGGT
 GTACAGGGGGCTGGCCCGAACTTTCATGAAGTTCATCCAGCTGTGAGCATCAGTACCTGTG
 TCTACGAGAAGCTGAGATCACCTCGGGCTGACGTGCGGCTGACGGGGGGAGGGGCCCCCG
 GCAGTGGACTCGCTGATCTGGGGCCGACGCTGGGGTGTGAGCCATCTCATTTGTAATG
 TGCCAAACATGAAGCTGCTCGAGGCCAAGTGTGAAAACCTTAGACGCAACCCGAGGAGGGT
 GGGGAGAGCTGGCAGGGCCAGGGCTTGTCTGCTGACCCAGCAGACCTCCTTGTGGTCC
 AGGGAAGACCAAGGCATTCTTAGGCTCAGGGTCAGCGAGCTCCGGGCTCACATGTGTAA
 GGACAGGACATTTTCTGAGTGCCTGCCAATAGTGAAGCTTGAGGCTGGAGGCGGCTTAGT
 TCTTCCATTTACCTTTGACGCCAGCTGTGCGCACGCCCCCTGCCCTTGGCTGCGCGTGC
 ATCTCCCTGTGCCCTTGTGCTGCTGCTGCTGAGTAAAGTGGGAGGAGGGCTACAG
 CCCACATCCCACCCCTGCTCAATCCCATATCCATGATGAAGGTGAGGTACGTTGGCCT
 CCCAGGCTGACTTCCCACTACAGCATTCACGCCAATTTGGCTGTGAAGGAAGGAAAG
 GATCTGGCTGTGGTCACTGCACTGTGACCTGTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTGCAGGGGCTCGGCTGCTGGCTGCTGCACAGAAGCAAGTGTGGGCTCA
 TGGTCTCTGAGCTGGCTGGACCTGTGAGGATGGGGCCCCACCTCAGAACCAAACTCACTG
 TCCCCACTGTGCAATGAGGCGAGTGGAGCACATGTTTGAAGGCGAAGGGCAGAGCTTTGT
 GTGTTCTGGGGAGGAAGGAAGAGTGTGGAGGCTTAATTTATGACTTTGGGAAAGGG
 TTTTGTCAAGAGCAAGCGCGGACAAATGAGCAGTCTCTGTGCTTCCAGAGGAAGAGCGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTCCAAC
 CCAGCAGGGGCGCAGCGGACAGGCCACATTCACCTTGTGCTGACTGTTGGAACCTTATT
 ATTTGTATTATTGAACAGAGTTATGCTTAATTTTATAGATTGTTTAAATTAATA
 TTTTGTGATTTCAAGTTCATTTTTTATATATTTATGTTGATGTTGATTTGACTTCC
 AAGCGCCCCAGTGGGATGGGAGGAGGAGAGAAGGGGGGCTTGGGCGCTGCAGTCACT
 CTGTCCAGAAATTTCTTTTGGGACTGGAGGCAGAAAGCGGCCAGAGGCGAGGCTGGC
 GCTCTCTTCTTTGGCAGTTGGGGAAGGGCTTGGCCCCAGGCTTAGGATTTCAAGGTTTGA
 CTGGGGGCTGAGCAGAGAGGAGGAGAACCTCAATAACCTTGAAGTGGAACTCAGTTATTG
 CTGCGTGCAGGGTTTCTTTTATTTCACTCTTTTCTGATGTCAAGGCAAGTGGAGTGCCTCT
 CACTGTGAATTTGTGGTGGCGGGGCTGGAGGAGAGGTTGGGGGCTGGCTCGCTGCTCC
 CAGCCTTCTGCTGCCCTGCTTAACATGCGGGCAACTGGGCAAGCTCAGGCTTGCATCTCC
 ATTTCCACAGAAATGACCTGATGAGGAATCTCAATAGGATCAAGATCAATGAAAAAAT
 GTTATATATGAACATATAACTGGAGTCGTCAAAAGCAAAATTAAGAAAGATTTGACGCTTAG
 AAGTGTTCATTTAAAGCAGCCTTCTAATAAAGTTGTTCAAGCTGAAAAAAGAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKNDRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI
 NVLKIAPESAIAKFMAIEQIKRLVGSQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG
 CAATTGCACTCATCATTTGGCTTTGGTATTTCAAGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTCAAGAGCCCGACAGCAGTGTTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGCTTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
 TGAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTCAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAA**AA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAAC TAGACAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGCGTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

208/330

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKNVQLTD
AGTYKCYIIITSKGKGANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

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FIGURE 209

[illegible]

0990441.13501

FIGURE 210

[illegible]

CTTCTGTAGGACAGTCAACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCAATGAAGGGCATCCTC
TTGCTGGTATCACTGCAGTGCTTGTGTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCCTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
GCTGAAGAACACATTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCCCTCCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTATTG
AATCTAATGGAATTCCTGTCTGTGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTCT
TTTCTAGTTGCGAAGCTTAAGAATGACATTGAGTCTAAGAGTCTCTGTGCTGAAAGGCTGTTT
CAACGTCTAGTAACGCCACCTGTCAAGTTCCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA
TCTTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCTGCACAACCACT
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
GGGACTGCTGCCCTGAGGTCTTGGGGCTGCACCTTGGCCAGCACCCCAATTTCTGCTTCTCTG
AGGCTCCAGAGCACCCCTCGGGTCTGCACACCTCTTCCCTGCTCTGCCCCGTTTAACTGC
CCAGTAAGTGGGAGTCACAGGCTCTCAGGCAATGCCGACAGCTGCCTTGTCTTCTATTATTA
AAGCACTGGTTTCATTCACCTGCCAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR
LYQNMFCSAENCSEETHITAFTHVHSAEEHFHFVSQCCQGKECNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFECANVNSLTPTSAPTTHNVGSKASLYLLALASLLLRGLLP

099044.1162

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
 GGGCTTGCTCTACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCGCCG
 GCGCGCTGCTGTGGGTCTGCTGAATCTGGGTCCCCGGGCGGCGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGCCGCTCACCCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCTGGGCACTGCCAC
 TCGAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGAGCACAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCGCCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAATATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

FIGURE 214

CCCGGGTCGACCCACGGCTCCGGGAGAAAGGATGCGCGGCTGGCGGCGCGGTGGTCTGCTAGCTGGGGCA
GACCGCTGGCGAGCGGCTCCAGGGCAGCTGTAGCCGCTGTACCGGACTCGGTATCGATGCGGAAGAGCA
GAACTGCTCTGGGGGCGCTGTAATCACTTCGGTCCCGCCAGCAACTACATGAGTTAGCAGCGCTGGACCT
CTCGGGACAGCTGTAAATATGAGTTATGTGGTCACTCGGTTGGGCTCTACCTCCAGAAAGGTCAAAAGTGCC
CAGTCTGATGCAAGTAGTGCCCTCTCCGGTTCTGTTCTTTAAAGACGGCATCGGCTCGGCTCGTTTCT
CAATGGCTGGCCAGCTGGTGATGCTCTCGGCTCAAGCGACCTCTGTGGCGAGCTCTCTCCCCATGTACCA
CTGTGTGGCTCTCGCTCGGTGTGCTTCAATGATGGTTTGTGTCAAGTTCTTCCACACAGGGAACCTGAT
CTACAGAGAAATGGACTACTCTGTGTGCTCCACTGTCTACATCACTCAATCTAGCTGTGCTGCTCGATG
CTGGGGCTCGAGCACAGGACTGTGTGATGCTGCTCCGGGCTCTCTGTGCTCATGCTGACCGTCCAGCTG
CTCTACTGAGCCATCATGCTCTGCAATATGGCTACAACCTGTGGGACAGTGGGATATGGGCTGCTCAACGT
GTGTGTGGCTGGCTGTGGCTGTGGAAACGCGGCGGCTGCTCACTGCGCAAGTGGCTGTGTGTGGTCTT
GTGTGTCGAGGGGCTGTCCCTGCTCGAGCTGTTCACTTTCCACCGCTCTTTGGGCTCTGGATGGCCATGCA
TTGGACATCAGACATCACTCCGTGACAGCTCTTTTACAGTTTCTGGAAGATGACAGCTGTAACTGTGT
AAGAACTCAGAGGACAAGTTCAAGCTGACTGAAGACCTTGGAGGAGTGTCTCCCCAGTGGGATCTGCCCC
GCGCTGTGGCTCTCTCTCTCCCTTGCACTCAACCTTGAGATGATTTTCTCTTTTCACTTTCTGAATTGGACATGA
AGGATGTGGGCGAAGATCATGTGCGAGCCACCCCTGTTGGCCCTCACCAGCTTGGAGTGTGTTCTAGG
AAGGCTCCAGCATCTGGAGATCTGAGAGTGGGACAGCCCTCACTCTGTGGAGCTGAATGGGGTAGCAATGA
GTGTGTTTATGCTCTACCGGGAGACAGCTGCTGTTCTCTCCCCACAGGCTCTCTCCCCATCTCCCGAGTGT
CTGTGCTGGTCTTGAGCCGCTCTGTCTCATGTGGAGACAGGGAACACAGGCTTAGGATACAGGGGCTCC
CTTCTGTACACACCCCTCCCTCTCTCCAGGACACCACTAGTGTGTCTGGATGTGTCTTTTGGCCAGCCAA
GTTTCACGGCTCTCCCATCTGGATCTTGAGGACAGCTGCTGGAGTGGGAAGGATTTTCACTGACCTGAC
GTGTGCTTACGAGCACTCCAGAGGCTCTCACATCACTCCCTTTCAGGAGTCAGGCTCAGCAGGCCAGGCA
AGATCTCTGTGTCTGTCTGTGTGAGGCTGACCCGTGTCTGGAGTGTGGGCGAGCTGAGTGTAGTATAGT
TGACAGGGCCCTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGTGGCGCATGTGGAGACGGGTGTGT
CGGGAAAGAGGTGTGCTTCAAAGTGTGTGTGTGAGGGGTTGGTGTGTGAGTGTGGGTTAGGGAAGCTGTG
TGCGCTGTCTGTGTGGGACTGTGAGATGAGTGAAGTCGCGGTGAATGTGTCCACATGTGAGAGTGTGGACAGGAT
GAGGAATCTCTGACCATCAATAATCACTGTGGAGCGCAGCTCTGCCCCAGACGCACTGGGCGGACAGC
CAGGAGCTCTCATAGGCAGGCTGCTGTGTGCTGTTCCCTGTCTGTGGCTCTTGGCCGCTCTCTGCAAA
CTACAGGGTCCCCACAGGAGTGCCCTCAGAGACAGCCCTCGGAGGACAGGAAGAAGAAATGGGATGCT
TGGGGCTCTCTCATCTCTCTTTCTCTGCTCTGCGATGTGGCTGGCCCTCTCCCTCAAACCTCTATCTCCCT
GTGCGACGCCCTTTGCCATAGCTGATTTTGGGAGGAGGAAGGGGCGATTGTAGGGAAGAAGGAGAAAGCT
TATGGCTGGGTGTGTTGTTCTCTCTTCCAGAGGCTCTTACTGTTCTCAGGTTGGCCAGGCGAGCGGGCC
ACCATGCTGCTGTGCGCTGTAAGTGAACCTGGCATTTTACAGACAGCCGGCATTTCTGCGCCACAGG
AATAGATGGAGGAGTCTCAGAAATCTTTCATCTCCAAAGGCGAGTCTCGCTGGTTGAAGCAGACTGATTTTTG
CTGTGCGCTGACCCCTGTCCCTCTTTGAGGAGGGAGGATCTGTAAGACTTCAACTCAGGAGCTCGGTTG
GCTCGGCTAGCTCTTTTGATACTGAAACCTTTAAGTGGGAGGGTGCGAAGGATGTGCTTAATAAATCAA
TTCCAGGCTCAAAAATTTTAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWFFSRFLFFQEPASAVASFLNGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDLDLTKMDYFCASTVILHSTYLCVVR
 TVGLQHPPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMNAQDLLSFGGLQVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRTLQVEKGTEVLAVRVVTTLLYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTGCAGTGGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCCTGTCTGGTCAAGGCCCCACCCCC
 TTCCCACCTTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGGTGCACCTTTCGTGCGCTTCGGC
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCGCTTCGCGTTATCATCTGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCTCGGCCCTCTGTGGTCTGGTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCTGATTTTTGGTGTCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCGCTTTGCCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACTTGGGCGAGGTGTGGTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTGTATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTGGGAGTCACTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCTTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCGAGCC
 TCTTGTGTAAGGACTGACTACCTGGACTGATCGCTGACAGATCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATCTCTGTCTCTCTTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCTGGGTTCAGCCAGTCACTGAGTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCTGTGTGTCAGTGTCTGTCTCTCAC
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGTCAGGCCGACGCGCAGGAGACAGTCCGGTGT
 GGTGTATTTCTGCCCTGCGCATCCCAACCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAGAAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTGGTCTTTTCTC
 AGGCCCTGAGGGGGAACCATTTTGGTGTGATAAATACCCATAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTAACCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAGTGCATGTTTGGGAACCTGGCATTACTGGAATAATGGTTTTAACT
 CCTTAACACCAGCATCCCTCTCTCCCCAAGGTGAAGTGGAGGGTGTCTGGTGAAGTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGTACCATGACATCGTAGGGAAGGAGG
 GAGATTTTTTTGTAGTTTTTAATGGGGTGTGGGAGGGGGGGGAGGTTTTCTATAAAGCTGT
 ATCATTTTCTGCTGAGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTGACT
 AATAAAAAAGAAATTTGAAAAA
 AA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPIYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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FIGURE 223

NGTTGGAGAAGTGGCGGGACNTTCATTGGGGTTTCGGTTTCCCCCTTCCCTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGTTTCGGCCCGGCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTIG
GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCGTGTGCGTCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGATGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAAGTTATGAATCTGGGC
 AGCAGATGTTCAGGGGGTCAAATCCATCCCCACCCCTGGTACTCCCAACCCTGGCCACTCT
 AACGACCTCATGCTCATCAAAGTGAACAGAAGAATTGCTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTTGTCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACCTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTTGGGGAGATTACCCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTCGAAGTTCACCAAGTGGAATCCAGGAAACCATCCAGGCCAACTCCTGAGTGCAT
 CCCAGGACTCAGCACACCGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCTCTCCAGAGATGTTGAGAATGTTATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGTGACCGGTGTCTCTAGTTGAACCCCTGG
 GAACAATTTCCAAAACTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAAGTGAAAAAAA

FIGURE 226

MATARPFWMWLICALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 227

ATGTCACACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGACCGGCCGCGCGA
 CAAGCCGACGCGCGGAGCTCGGCTACGTGCTGTGCACCGTGTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTGCACCGGTGCCGTGCTCTTCTGAACACCGCCACCGCCGCGGACAG
 GCGCCCCCACTGTCTGCACCGGTGGGGTGGCAGCGCCAAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCAGCTCAGCATCTCTATTGACCCGCGCTGCCCGAGCTCACCGACA
 GCTTCGCACGCTGGAGAGCGCCAGGCCCTCGGTGCTGCAGGCGCTGACAGAGCACAGGCC
 CAGCCACGGCTGGTGGCGACACGAGAGCAGGAGCTGTCAGACGGTGGCCGACAGCTGCC
 CCGGCTGCTGGCCCGAGCCTCAGAGCTCGAGACGGAGTGCATGGGGTGGCGAAGGGGATG
 GCACGCTGGGCCAGGGGCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCT
 TCTGAGAGGACAGGGCCATGGCTCACCTCGGTGAATCCGTGACGGACATCTGGATGCCCT
 GCAGAGGAGACGGGGCTGGCCCGGCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGAACCGGCCCGGGGCTGTGCCACTGGCTCCCGGCCCGGAGACTGTCTGGACGTCTCT
 CTAAGCGGACAGGAGGACGATGGCTGTACTGTCTTCCCAACCACTACCGCGCGGCTT
 CCAGGTGTACTGTGACATCGCAGGAGCGCGCGCGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGGCTTCTTCCGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAGAGGATCCAGCGCTGACCAACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGAGCTTTGAGAATGCGACGGCTATGCCGCTACGGGAGCTTCGGCG
 TGCGCTGTGTCTCGCTGGACCTGAGGAAGACGGGTACCGCTCACCGTGGCTGACTATTCC
 GGCACCTGCAGGCGACTCCCTCCTGAAGCAGCGGCTAGGTTTCAACCAAGGACCGTGA
 CAGCGACCACTCAGAGAACTGTCCGCTTCTACCGCGGTGCTGGTGGTACCGCACT
 GCCACAGCTCAAACCTCAATGGGCTGCGCGGTGCGCACGCTCTTATGCGGAGCGG
 TGGAGTGGTCTCTTGAGCGGCTGGCAGTCTCACTCAAGTTCTCTGAGATGAAGATCCG
 CGCGGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGTGGTCCCTGTGCG
 CCCATCCCCGACCCCACTCACTCTTCTGTAATGTTCTCCACCACTGTGCTTGGCGGAC
 CCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGCGCGGTGAAGT
 CACACATCGCCTTCTCGCGTCCCGACCGCTCCATTTGGCAGCTCACTGATCTCTTGCCTC
 TGCTGATGGGGCTGGCRAACTGACGACCCCACTCTGCTGCTGCCCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCTGGCCAGGATGTTGAGTCTGCCCGAGGCACTCTGCGCTGCCG
 GGCCAAATACCGGCATTATGGGACAGAGAGCAGGGGCGACAGCACCCCTGGAGTCTCTC
 CTAGCAGATCGTGGGGAATGTCAAGTCTCTCTAGAGTCAGTCTGAGGCCAGTATCCCTCAG
 CCTCCCAATGCCAAACCCACCGCTTTCCCTGGTGGCCAGAGAACCCACTCTCCCCCAA
 GGGCTCAGCTGGCTGTGGGCTGGGTGGCCCATCTTACAGGCCCTGAGTGCAGGATGGG
 GAGCTGCTGCTTTGGGACCCACGCTCAAAGGCTGAGACAGTTCCCTGGAGGCCACCCAC
 CTTGTGCCCGGAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGTCTCTGTG
 TCTCAATAGGGCCCAACCACTCCCGCCACCACTCCCGGCCGTCTCTACCTGGGGCAGC
 CGGGCTGCCATCCATTTCTCTGCTCTGGAAGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCGCTAATGGAGCTTGTGTTTTCTGGGCTGGGGCTAGGACGGCTGGGATGAG
 GCTTGTACACCGCCACCAACCAATTTCCAGGAGTCCAGGGTCTGAGGCCCTCCAGGAGG
 GCTTGGGCTGATGACCCCTTCCGAGGCTGCTGTCTCATGAGGAGGCCAACCTTGCC
 ATTGACCGTGGCCACTGACCCAGGCCAGGCCCGGCCCGGCGAGTGGTCAAGGGACAGGGA
 CACTCTCACCGGCAATGGGGTGGGGGAGTGGGGCAGCAGACAGGACCACTGGACA
 TCTTCTTGTGTAATCTCCCAACCCAGCACGCTGTCACTCCCACTCTTGTGTGACACA
 TCCAGAGTGAGACCCGAGGCTCCAGGACAGCCAGCAGGACAGGCGAGGCTGGAGCGGG
 TCTCAGCTGTCTCTCAGCAGCCCTGGACCCGCTGCTGTACGTGAGGCCAGATGACAGG
 GCGCTTTTCAAGGCTCTGTATGGGGGCTCCGAAAGGGTGGATGAGCTTGGGAGCT
 GCTCAGCAGCTCTCTCTCGGCGAGGAGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GTGCTCGTAGGGGTGTGGGGTTCGTTCTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACAAATAAATTTGACTTGGCACCACTGGGGGTTGGTGGGAGAGGCCGTGTGACTTGGCTCTC
 TGTCCAGTGGCCACAGGTTCATCCATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKXSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

000000-1150

FIGURE 229

GCAGTCTCAGAGACTTCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT
TGCTTCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCT
CACCCTGTAGGAATCCAGATGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
CGGCGCACAGAGCACAGGGCTCCCCTTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGAC
TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACC
AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
GACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAACAAGAAGA
CCTGGAATTTGCCGCTCTCAGAGCTACTCTAGTTTTCTACTCTTATTGGACAGGGCTTT
TGCGCCCTGACATGAGTGGCAGGCTGGCTGTGGATGGAAGCCCTTTTCACTTCTGAACTG
TTCCATATATATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCTCAATGG
GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCCGC
CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCTGTG
TTTCTGTTCCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCAGTATTTAACAGTCACA
AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCAFTGCTTCTGTG
GCTTAGAGATAACTTTTAGCTCTCTTCTTCTCAATGTCTAAATATCACTCCCTGTTTTCAT
GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTTGGCAGTCACTTCCCAGATTGTACC
AGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
AATCTCAAACTCTCAATGCCTTATAAGCATTCCTTCTGTGTCATTAAAGACTTGATAATTG
TCTCCCCTCCATAGGAATTTCTCCGAGAGAAAGAAATATATCCCATCTCCGTTTCATATCAG
AACTACCGTCCCCGATATTCCTTCAGAGAAATTAAGACCAGAAAAAGTGAGCCTCTTCA
TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTTCAG
GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKL
LYNKAGAHRCSPCTEQWKWHGDNQYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLE
FAASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRPSRDCVAIL
NGMIFSKDCKELKRCVCERRAGMVKPESLHVPPETLGEGD

000001.11601

AATTTTCACCCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATAAAGCTTGACGGAAGTNTGCAGCAT
GTGGCTGAAAAACTGTCTGCAGTCACTGATAACAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCATTCCC

FIGURE 232

GCCGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCTCCCGGGTCCCGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTTCGCCGGGCGGGGACCCGCGGTGCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCCTGAGCCT
 GCTCAGCGTCACTGGTGGAGGAGCCGTGCGGCCCGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCGCGCGGCAACACCAACGCCGCGCGCCGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGGCCGGCGAAGGCGCCGGGAGAAATGGGAGCCCGCGCTTTGCC
 CTACCACCCTGCACAGCCCGCCAGGCCGCCAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCAAGCTGCC
 ACGCTGGGCGTGCCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCACGGGGCCCGCGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCTGCTGCTGACACCACCTACACCGAGGCGCACGGCCTGGCACGCCCTAACTGG
 CCACCTCAGCCTGGCCTCCGCGGCCACCTGTACCTGGGCCGGCCCGAGGACTTCATCGGCG
 GAGAGCCACCCCGCGCTACTGCCACGGAGGCTTTGGGGTGTCTGCTGTCGCGCATGCTG
 CTGCAACAACTCGCCCCACCTGGAAGCTGCCGCAACGACATGTCAGTGCGCCCTTGA
 CGAGTGGCTGGGTGCTGCTTCTCGATGCCACCGGGGTGGCTGCATGGTGAACACAGG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGCAAGGAGGGGACCTCAT
 TTCCGAAGTGGCCTGCAGACCCACCTGTGCGTGAACCTGTGCACATGTACACCTGCACAA
 AGCTTTTCGCCCGAGCTGAATGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATAACAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT
 CCAGACCACTCCCGCCCGGCCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCGGGGTATGGA
 ATACACGCTGGACTGTGACCTGGAGGCACTGACCCCGAGGAGCGCGCGGCCCTCACTC
 GCCGAGTGCAGCTGCTCGGGCCGCTGAGCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCAGTCTCACTGTGCTGCTGCCCTTAGCTGCGGCTGAGCGTGACCTGGCCCTTG
 CTCTTTGGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCACGCCCTGACCC
 TGCTGCTACTGTATGAGCGCGGCCAGGCCAGCGCTGGGCCATGCAGATGTCTTCGCACT
 GTCAAGGCCACGCTGGCAGAGCTGGAGCGCGTTCGCCGCTGCCGGGTGCCATGGCTCAG
 TGTGCAGACGCCGCACCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGCG
 TGGACACACTGTTCTGCTGCGCGGGCCAGACACGGTGCTCAGCGCTGACTTCTGAAACCGC
 TGCCGATGCATGCCATCTCGGCTGGCAGGCGCTTCTTCCCATGCATTTCCAAAGCCTTCCA
 CCCAGGTGTGGCCCCACACCAAGGGCCTGGGCCCCAGAGCTGGGCCGTGACACTGGCCGT
 TTGATCGCCAGGCAGCCAGCGAGGCCCTGCTTCTACAACCTCCGACTACGTGGCAGCCCTGGG
 CGCCTGGCGGCAGCCTCAGAACAAAGAAGGAGCTGCTGGAGAGCCTGGATGTGTAGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGGCCACGAGCTGCAGCGCAGGCTCAGTGAGGACCTGTACACCGCTGCCCTCCAGAGC
 GTGCTTTGAGGCGCTCGGCTCCCGAACCCAGCTGGCCATGTCTACTTTTGAACAGGACGAGG
 CAACAGCACCT**GA**CGCCACCTGTCCCGTGGCGCTGGCATGGCCACACCCACCTT
 CTCCCCAAAACAGAGCCACCTGCCAGCTCGCTGGGCAGGGCTGGCGTAGCCAGACCC
 AAGCTGGGCCACTGGTCCCTCTCTGGCTGTGGGTGCCCTGGGCTCTGGACAAGCACTGGG
 GGACGTGCCCGCCAGGACCCCACTCTCATCCCAACCCAGGCTTTCCTGCCCCCTGACGCT
 GCTGATTTCGGGCTGTGGCCTCCACGTATTATGCAGTACAGTCTGCTGACGCCAGCCCTGC
 CTCTGGGCGCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGGAGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCTGCCGAAGCTCCTGCTTTAATAAAGTGGCCA
 AGTGTGGA AAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDDEFDWFFLVPDTTYEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFERSALTAHPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAAEQEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEQQNST

GCTCTGGCCGCCGCCGCGCATTTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
TGGCAAGCGCTGGCCACCTCCCCACACCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTCCGCAGGGCCCGCTTTTTAGAACTTGATTTCCTTTGAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCAGGGAACTCGGGGCGATTGGCTGGGAA
CTGTATCCACCCAAATGTCACCGATTTCCTTCTATGCAGGAAATGAGCAGACCCATCAATAA
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
AGGGTTGCTCAACGCCCCCGCCTCATTTGAAAAACCAATCAGATCTGGGACCTATATAGCGTG
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
TTCCCGCCCTGAGACCCTGCAGCACCATCTGTCA**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
GCTCGCCGCTTTTTGGCGGCAGCGCGCAGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCTGTGGCGGGAAAGCGGCCCCAGAAC
CGACCACACCGTGGCAAGAGGACCCAGAACCAGGACGAAAACCTTGATGAGAGAACC
GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGCTCTTCT
CTTTGGCGTCTCCATCATCTTGGTCCTTGGCAGCAGCTTTGTGGCCATATCGCTGACTACA
GGATGAAGAAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAATAACCGAGGCCAATGGC
CTTCCCATTATGGAATCAACTGACTTTCGACCCAGCAAGATCAGGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

235/330

FIGURE 235

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

099044.11601

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCACGCGAGGGC
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCAGAACCGACCACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGCTGCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCACTTACACAAAGGCTTTTGGAGGACCCGATACCTGGGGGCCACCCCTCCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTTGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACAGCTACCACTCCCAAGGAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTGAGTTGTATTGTATGTCCTTC
 ATCAGCGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTACCGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCATACATATCAGGACGTCATCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTGTGTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCGAGAGAAATGAGGCCCCCAAGTGCCTCTCCCTGC
 ATGCCCGAGCGGTACGTGAGTGGCTATGGGCTGCAGAGAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCCTCCCGGTGCTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACTCCAAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTCACTGCGCG
 GCCAAGCTCAGTCAACAAGGTTTCCATCCAGTTTGTAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACCGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCATGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTACCCGAACCTTCCACATCGAGGAGCCCGCACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**TGA**TT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACAGGTCAGGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTA
 CTAGAAATTCATTTCTCACTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCCGTGGCTGCTGATTGGACAGCACAGAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTTCCGTGGAAAAA

0090441.1.1667
 TGGTTT.1440660

FIGURE 238

MPLALLVLLLLGPGGWCLAEP PRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTL SVVFDAFITG
QGKKDWSLFRMF SRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFFVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVS IQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLL VNLPTPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATGAATGCTGGGTCTTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGTCTCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGCTAGAAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

099044-11001

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEggnKDEdVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCAC**ATG**AGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAAGG
 CGTCCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTCTTCTGCTTGCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCAGGCAACCCAGAGGGGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGCCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGACGACCCAAGGAATGGGGGCCAGACCAGGAAGCTGACGGCTCCAGGAGC
 GTGTCAGAGAAGCACCGGGGCAAAGCGGCAACACAGCCAAAGACGCTCATCCCAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAGGAGTGACCA
 CAGCAGTCTATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTTGCCCTTTCCAG
 AGCCCCACGACGACAGAACCCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGGCCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAAACTCTTTCTGCCAACCTCACTCTC
 TTTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCCCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCTTGGTGCGAAGGTGTCGACACGCTTCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCACTACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTATTAAAGGCTACGAACAGGATGTGGGACTC
 GGACATCCTTCTACGGCTTACC GCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTCAGAACAGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCTCGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAAATCCGGCTGTACCAGCGCTCCGGTC
 CCGGAACCTGCCAAAGCCAAAGAC**TGA**CCGGGGCCAGGGCTGCCATGGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCTGGGTGAGCTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTTCTGAAGTCTTCTCAGTACATTGCTGAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGACTTCG
 GTTGAATTCCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACCTCACTAC
 AGATTGCTAGAAAGACCTTTCTAGGAGTTATCTGATTAGAAGGCTATATACTGTCCCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAAGGCAATAAATTTTCTACAGTGAIAAAAAAAAAAAAAA

00000441-11660
 11660-11660

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQLHRMLAPTGAIVSTRTRQKGVTTAVIPPKEKKQATPPAPFQSPPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTFRFPVPQQQLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
 RYMKNRFLRSKTLDGAWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTST
 KRLIFYINHDFKLEREVWKRHLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

FIGURE 245

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGGTCTCGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCACCAATGCCACCCGCGGGGCTCCGCCGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGTGGGGGCTCCCCCTGGTGTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATACCGAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
 ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTCAAATAGTCCCTCTGCTCCCAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT
 TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAPLTAIALLVLGAPLVLAGEDCLWYLDNRGSHWPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCCAGGTAGGTTAGGCAAGAAAGATGGTGTCTTTCGCCCTCAAAATGGTCCCTTGCACCACTG
 TCATTTCTACTTTTCTCACTGTGGCTCTCTTAACGTGTGCCACTCCCTTCATGGTGTACAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTGGAAATAAAATACGACTTC
 CTGACTAGCTCATCCCAGTCTATTATGATCTCTTGATCCATGCAAACTTACCACGTGACC
 TTCTGGGGGACCAACGAAAGTAGAAATACAGGCCAGTCAGCCCCACGACACCATTCCTGCA
 TAGTCAACCTCCAGTATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGGGCTATCCG
 AAGAACCCTGCAGGTCTTGGAAACCCCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG
 CCCCTCCTTGTGCGGGCTCCCTACACAGTTGTCACTATGCTGGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAACACCTACAGAACCAGGGAAGGGGAACCTGAGGATACATGACAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTCCCTGCCTTGTATGAACCTGCCCTT
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTCAAGCAAGATAACC
 AAGATGGAGTCAAGGTTTCTGTTTATGCTGTGCCACAGAAGATAAAATCAAGCAGATTATGC
 ACTGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTTATTCAGCATACCGTATCCCC
 TACCAACAATAGAGATCTTGCTGCTATTTCCGACTTCAGCTGGTGCTATGGAAAACTGGGGA
 CTGACAACATATAGAGAACTTGCTCTGTTGTTGATGCAAGAAAGCTTCTTCGATCAAGTAA
 CTTTGGCATCACAGTGACTGTGGGCCATGAACCTGGCCACCAAGTGGTTTGGGAACCTGGTCA
 CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG
 TCTGTCACTGTGACCAATCCTGAACTGAAAGTTGGAGATTTATTTTGGCAAAATTTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCCTGTGTCTACACCTGTGGAAAACTCTG
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTTGATTTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGTGGTATTTGACAGTATCTCCAGAAGCA
 TAGCTGTAAAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG
 ATGGTGTAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTTTCATCTTCATCTCACAT
 TGGCATCAGGAAGGGGTGGATCTGAAAAACATGATGAACACTTGGACACTGCAGAGGGGTTT
 TCCCTTAATTAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGCGCCCGGACACTGGGTACCTGTGGCATGTTCCATTTGACATTCATCAC
 AGCAAACTCAACATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCC
 AGAAGAGGTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTGCAATTACG
 AGGATGATGGATGGGACTTTTGACTGGCCTTTTAAAGGAACACACACGAGCAGTCAAGAGT
 AATGATCGGCAAGTCTCATTAACAAATGCAATTCAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAATAAGGCTTGATTTATCCCTGTACTTGAACATGAAGTGAATTTATGCCCGTGTGTTT
 AAGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAACTCAATTTAAGGGCTTCTCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACCTACTCTCTCGCCTGTG
 TGCACAACTATCAGCCGTGCGCTACAGAGGGCAGAAGGCTATTTGAGAAGTGGGAAGGAATCC
 AATGCAAACTTGAGCCTGACCCTGTGCGAGCTGACCTTGGCAGTGTGTTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTCTTTATAGTAAATATCAGTTTTCTTTGTCCAGTACTGAGAAAA
 GCCAATTTGAATTTGCCCTTGCAGAACCCAAATTAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATTTCTACACTCATTTGG
 CAGGAACCCAGTAGGATCCCACTGGCCTGGCAATTTCTGAGGAAAACCTGGAACCAAACTTG
 TCAAAAGTTTGAATTTGGCTCATCTTCCATAGCCACATGGTATGGGTCAACAAATCAA
 TTTCTCACAAAGAACACGGCTTGAAGAGGTAAAAGGATTTCTCAGCTCTTGAAGGAAAATGG
 TTTCTCAGCTCCGTTGTGTCCACAGACAGATGTGAACCATTTGAAGAAAACCTCGGTTGGATGG
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAGGTGAAAAGCTTGAACCTATCTTAA
 TCTCTCCCTTGGCCGGTTCCGTTTATCTCTAATCACCACATTTTGTGTAGTGTATTTTCAA
 ACTAGACCTGTGAAAGAAATAGCTGTTAGTTTTTCATGAATGGGCTTTTTTCATGAATGGGCTA
 TCGCTACCATGTGTTTTTGTTCATCACAGGTGTTGCCCTGCAACGTAAACCCAGTGTGGGT
 TCCCTGCCACAGAAGATAAAGTACCTTATTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 249

CAGGCCACAGACGGGTG**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCTCCCACTGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAAGCTGGTGTCTCTCCAAGGGTGCACGGAGGCCAAGGACCAGGAGCCCGCGCTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATTCCTTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGCCCCACAGCCCCCAGCAGACCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGTGTCTGGAGGGGACAACAGAAAGAGATCTGCCCAAGGGGACCACACACTGTTATGATGGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGGTGCAACCTGTCTAATTGGGACACAGGAAGATGGCCCTGGTATGACTGAGA

ACTGCAATAGGAAAGATTTTCTGACCTGTATCGGGGAGCCACCATTTAGCATGACACGGAAACCTTGCGTCAAGAACCCACTTATTTGGACACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAGGTGTGCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCATCCACTCAGCCCTCCTGGGGTGTCTGTGGCCTCCTATACCACCTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCCCTTGGAACTGTTCAGTGGTCCCCCGAATGACCTGCCCGAGGGCGCCACTATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGTCTCTTGTGTAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGACACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTCACATTCTGTCATGAATCACTTCCCCACACAAATCATTCATCTACTCACCTAACAGCAACACTGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGACGCTGGAGGAGTGGCTGATGTATCTGATAATACAGACCTGTCTTTCA

SECRET

FIGURE 251

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
 CAGC**CATG**AGGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGACGCTGAGCATGCCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGCGCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGACTGCGTGGAGATGTTGGCCT
 CGGGGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TCA**AGCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGAGCTGTCCCTCTGTGAAGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

MRGNLALVGLVSLISLAFSLPSGHQPAGDDACSVQILVPLKGDAGEKGDKGAPGRPRGVG
PTGEKGMDSGDKGQKGSVGRHGKIGPTGSKGEKDSGDTGPPGPNGEPLGPCESQLRKATIGE
MDNQVSQLTSELKFIKNAVAGREVETESKIYLLVKEEKRYADAQLSCQGRGGLTSMPKDEAAN
KLMAAYLAQAGLARVFICINDLEKEGAFVYSDHSPMRTFNKWSRSGEPNNAYDEEDCEVMVAS
GGWNVDACTHTMYLMEFIDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCTTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCAGAAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTCTACCTGACCTGGTGTGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTTAGAGTTCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTCCCGCTGTCTACCGCTGTCTGCTGGACGCGGGAGACGCGCAGCGAGCTGGTGATTG
 GAGCCCTGCCGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCGTGAGTCC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCTGGGTGGTGTATCCCCCTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACCTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCAGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCGAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGAGTCCTTCTCGCTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGAAAGGAGCTAACGGTGACAGAAGACAGCAAGGTCAACCCCTCCCGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGAAACTTCCTTCTTGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCACTATGAATGGCTT
 TTTAAACAAACCCACGTCCAGCCTGGGTAACATGGTAAAGCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

FIGURE 256

MSCVLGGVIFLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGAACTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCTCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAGCTCTGCCTCCTCTCCATCTCCCTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCTG
TGTCCTTCTTGGCCCGGGCTTTTGGCCGGGGATGCAGGAGGCAGGCCCCGACCTGTCTTT
CAGCAGGCCCCACCCTCCTGAGTGGCAATAAATAAAATTCCGTATGCTG

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FIGURE 258

MSGGLPLVLLLTLLGSSSHGTGPGMTLQLKCLKESFLTNSSESSFLELLEKLCLLLHLPSGTS
VTLHHARSQHHVVCNT

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FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTC CCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAATAAACCAATTATGTTTGTAATTGATTAATAAAAACCAGA
ATAAAAGTTCATATCTAGCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

10911 1400660

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAAGGAAATGGTGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCCTGTCAGCTTTTTCTGCCCCGCCAGTGTAC
 CCAGGACCCAGCCATGGTGCAATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAAGCAACGAGGGGCATACATTCAAGAATTCGAAGAGTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTT
 GGCACGTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTTATAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAAACCAAGCCAGCTCCCCGGAAGCAAACTCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAGAGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACTGTCATCTATGATCCACTGGGCACATCAGTGAGGAGCACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCTGGAATGAAGGAAACAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCCTCTGAAGTAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTT
 TACAGGACAGTGAGGCTATAGCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGAATAACGTATGCCTCTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTGTTTTACT
 GCTCCCCAGCATTACTCTGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAG
 CCTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAAATATTCTTT
 CTTTTCTTTTCTTTTTTTTGGAGACAAGGCTCACTATGTTGCCAGGCTGGTCTCAAACTCC
 AGAGCTCAAGAGATCCTCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAATACTATTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTC
 TCTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTGTCACATCATTTGAATTTCTGTTTCACTTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAAATACAAGTGAAAGATACAGC
 TAGAAAAATCTACAATAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTTCAGCCTAAAAATATAGTCTGTCCC
 TTTAGCAGTTTTTCATGTCGTCACAAGACCTTTCAATAGGCCTTTCAAAATGATAATTCTCC
 AGAAAAACAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTGTCTGTCTGCTCTGTCTGT
 TTCTCTCTTTCTGCTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

00990441-11501

FIGURE 263

GGGGCGCCGCGTACTACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTCGCAGA
 TGTGCGAGCTCATGGGGCTGTGCGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGCGCCCGCTTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACACAACCTTCAACCACCGCCTCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCAGCA
 TGAGAGCCAACTGGAGCTGGACCAGCCACCTGGTGCAGCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCGTGTCTTCAAGATGACCAAGCGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAAGCGCCTGTCA
 TCGACATTTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCAACACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGGAGTTCAGGAGGTGGTGCAGCCTTCGAA
 CTAAGGGGCCACTCCGCGGCTGTGCACTCGTTTGCTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGCGCGCGGTGCGCCGCTGCGGC
 CTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTATCTTA
 CAATACCCGGCGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCTCTGTGGGACCGGGCGGTGCGGCTG
 TTTACAACACTCTCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCTGA
 AGAGCCTGGGTGCCCTGAAGAAGTGACTCTGGGAGGGCCCGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCCTCTCATGGCACTGCTGCCATCTTTCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCCAAGGTGCTTTTCTTC
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAAATGTGATTTTGGCCTTGTGGCAGCACATCTCACACCCCAAAGAG
 TTTGTAATGTTCCAGAACACCTAGAGAACCTGAGTACTAAGCAGCAGTTTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCCATCAGAACTGTGTTCCATCAAAAAGCACTAAGGGATT
 TCCTTCTGGGCTCAGTTCTATTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAAGAT
 AGTACTATTGTCCAATGTCAATGAAAGTGGTAAAGTGGGAACCACTGTGCTTTGAACCAAA
 TTAGAAACACATTCCTTGGGAAGGCCAAGTTTCTGGGACTTGATCATACATTTTATATGTT
 TGGGACTTCTCTTCTGGGAGATGATATCTTGTAAAGGAGACCTTTTTCAGTTCATCAAG
 TTCATCAGATTCTTGGTGGCCACTCTGTGCCAAATAAATATGAGCTGGGGATTAAAAAAA
 AA

00990441-11571
 11571

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVEKMTKREDGGYTFTATPEDFPPK
HKAPVIDIGIANTGKFIMTASSD TTVLIWLSLKGQVLSTINTNQMNNTHA AVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSA AVHSFAFSNDSRRMASVSKDGTWKLWD TDV
EYKKKQDPYLLKTGRFEEAAGA APCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGH LKRASNESTRQR LQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTGTTTGCCTTACCCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACCTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCTTCTTCAGGAAACGCA
AGCACCACACCTGTCTTGTCTTGCCTAACCTGCTGTGCTCCAGETTCGCGGACGCGAGGTAC
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGGCTTGCCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCAGCAGCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCAGTCCCTACACTGACTACCTGATCTCTCTTGCTAGTAGCGACATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
CTGTGGTGTAAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTCCCTGGGCCCTG
CCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG
ACCAATTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGGCCAATCAGCCCCCTGAAGACTCTGGTCCCACTCAGCCTGTGGCTTGTGGCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTTACCACACTTTACAGT
TAACCACTGAAGCCCCCAATTCCCACAGCATTTCCTATAAATGCAAAATGGTGGTGTTCAA
TCTAATCTGATATTGACATATTAGAAGCAATTAGGAGTGTTCCTTTAAACACACTCTTTC
AGGATCAGCCCTGAGAGCAGGTGTGGTACTTTGAGGAGGGTCACTCTCTGTCCAGATTGGGG
TGGGACGACGGGACAGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

266/330

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGGCGCCGGGCGTCGGGGCGGTAAAGGCCGCGCAGAAGGGAGGCACCTTGAGAAATGCTCTTTC
 CTCCAGGACCCAAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGCG
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAACACTGGAGAAGGAACCAAGGACTTTCAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCACGCCATTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTATCCGTCTGGGAGTGTGTACAACTTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCAGAAAAAGAAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT
 GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGGGAGTCTGCAGAACCCGCTGAGCAACATGGCGAAACCCGCTC
 TCTACTAAAAATACAAAAATCACC GGGTGTGGTGGCAGGACTCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAAATCACTTGAACCTGGGAGGTGGAGGTGCGGTGAGCTGAGATCA
 CACCAGCTGATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFGFILGGVFV
VGSGKQGILHEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCAGAGA
AGCCCCCTTCCTGGGCGCTGCCAACC CGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGGCGCTGGGCCTGCCGTTCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLRLRWRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLRKQRTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

090044.11301
T03111.14406660

FIGURE 271

AATATATCATCTATTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAATGACATTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

TGTATTTAGGAG

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

[illegible]

FIGURE 273

GCCAGGAATAACTAGAGAGGAAC**AATG**GGGTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCCTGCTGCACAGTCAAACTACTTCTTCATTAAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTCATTCTTATAGATCCTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATATCTCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAACATG
 AAAACCATTAACATCTGCTGATGTTATAGTTGCACCACCTACACTCCAGCTAGAGATGAACCA
 TACACCAAGCAGTTTACAGAAATGTGGAGAGAAAGCCGAATACATTCACCTCACCCCTGACCT
 TCTACTTGGAAAAAAACAAATGAATGTGGACCACCAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGAAG
 TCAAAAAAATCAAGACCAACAGGTGTTCCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCGAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAACTGTATG
 GAAAAGATTGTCAATCTTTCTGTATAAAGTACAAAACAGAAAGCATCCATAATGTTTATG
 CAAAGATTGATCTGTGTTGAATTTTGTAAACGAAAAACCAATCAAGAAAGCTCCAAG
 CCTACRAAACATAAAGTCAATTTTGAAGTACATGGGAGGTGATTAGCAATCTGAGGATT
 TTA AAAACACCATACCCATGGTGACACCCACTCTCCACCTGTCTTCTATTGCTGAAGATC
 AGTCAAAAGATTGTGTGCTTAGTCTTGATAAGCTTGGAAAGCATGGGGGGTAAAGACCGCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTCGAGACTTTGAAAATGGATCTCTGGG
 TGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAATAAGCTATCCAAATAAAAAGC
 AGTGATGAAGAAGAACACACTCATGACAGATTACCTACATATCTCTGGGAGGAACCTTCAT
 CTGCTCTGGAATTAAATATGCAATTCAGGTGATTGGAGAGTACATCCCACTCGATGGAT
 CGGAAGTACTGCTGCTGACTGATGGGAGGATAACACTGCAAGTTCTTGATTTGATGAAGTG
 AAAACAAAGTGGGGCATTTGTTCAATTTATGCTTTGGGAAGAGTCTGATGAAGCAGTAAAT
 AGAGATTGAGCAAGATAACAGGAGGAAGTCAATTTTATGTTTCAGATGAAGCTCAGAACAATG
 GCCTCATGATGCTTTTGGGCTCTTACATCAGGAATATCTGATCTCTCCAGAAATCTCCTT
 CAGCTCGAAGTAAAGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCAAT
 TGATAGTACAGTGGGAAAGGACACGCTTTCTTCATCACATGGAACAGTCTGCCTCCAGTA
 TTTCTCTCTGGGATCCAGTGAACATAATGAAAAATTCACAGTGGATGCAACTTCCAAA
 ATGGCCATCTCAGTATTTCAGGAACATGCAAGGTGGGCACTTGGGCATCAACTTCAAGC
 CAAAGCGAACCCAGAAACATTAACATTACAGTAACCTCTCGAGCAGCAAAATCTTCTGTGC
 CTCCATCAGATCAATGCTAAATGAATAAGGACGTAAACAGTTTCCCAGGCCAATGATT
 GTTTACGCAAGAAATCTACAAGGATATGTACCTGTTCTTGGAGCAATGTGACTGCTTTAT
 TGAATCACAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGGCGTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAAATCTGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAAATACGGGCTCCCAT
 GAATAGAGCCGCGTACATACAGGCTGGGTAGTGAACGGGAAATTAAGCAAAACCCGCCAA
 GACCTGAAATTTGATGAGGATCTCAGACCCTTGGGAGGATTCAGCCGAACAGCATCCGGA
 GGTGCATTTTGGGTATCAAGAGTCCCAAGCCTTCCCTGACCAATACCCCAAGATGCA
 AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATCTTACATGGACAGCACCAG
 GAGATAATTTTGAITGGAAAAAGTTCAACGTTTATATCATAAGAAATAAGTGCAAGTATCTT
 GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGA
 GGCCAACTCCAAGGAAAGCTTGCATTTAAACCAAGAAATCTCAGAAGAAATGCAACCC
 ACATATTTATGCCATTAAGATATAGATAAAAGCAATTTGACATCAAAGTATCCAACATT
 GCACAAGTAACTTTGTATCTCCCTCAAGCAAACTCTGTATGACATTGATCTCACCTACTCC
 TACTCTCTACTCTCTCTGATAAAAGTCATATTTCTGGAGTTTATATTTTCTACGCTGGTAT
 TGTCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTATTTAAGTACCACCATTTGAACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAAATGTAAGT
 AAGAGATATTTCTGAATCTTAAATATTCATCCCATGTGTGATCATAAACTCATAAAAATAATT
 TTAAGATGTCGGAATAAGGATACTTTGATTAATAAAAAACACTCGGATATGTA AAAACT
 CAAAGATTAATTTTAAAGTTTCAATTTATTTGTTATTTTATTTGAAGAAATAGTGATGAAC
 AAGATCTCTTTTTCATACTGATACCTGGTTGTATATTTATTTGATGCAACAGTTTTTCTGAAAT
 GATATTTCAAATTTGATCTCAGAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAA
 GGAGAGCAAAATAAACCAACTTTGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 274

MGLFRGFVFLVLLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFKNVSIIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFFYRAKSKKIEATR
 CSAGISGRNRVYKCGGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDfKNTIPMVTPPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIIQIKSSDERNTLM
 AGLPTYPLGGSICSIGIKYAFQVIGELHSQLDGSEVLLLTGDGDNNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDBGVYSRYFTAYTENGYSCLKVRAHG
 GANTARLKLRLPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDfSRASGGAFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGKVGQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNNIAQVTLFIP
 QANPDDIDPPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTCGACGAAAGACGGGAAAGACCATTACGTCCTCCC
CGAGGGGGTGACACACGGTGTCTCTCTTTGATCTGCTGTGGCTGGCTCTCTTCTTATCAAGAAAG
ACCGTCAAGGTATGCTGCTGACAGAGCAATGATGTACCAACCTCTTAACCTTCTCCCTTCTTGAACC
CCGAGTCTGCTGACGAGTTTACTAGAGGCTGTCACTCAACCAAGCAAGCGGGCTCTTCGGCTTAACTT
CTGCTTGACGAGAGAACTTTGTGGGGCTGGCTTCTTTAGGATGCTCAGAAGTGACTTGCCTGA
GGCTTGACCAAGAGAAAGGAAAGCCCTCTTGTCTGTGCTGCATACAGGAAGGCTGTGATGGG
AATGAAGCTGAAACCTTTGGAGATTTCACTTCACTTCAATGTCTTGCCTCGAAGATCATCTTTTAAAA
GTAGAGAAGCTGCTCTGTGTGTGTGTTAACTTCAGGAAGGCAAGACTCGTTCTAGAAGAAATGGATG
CAAGCAGCTCCCGGGGGCCCCAACCGCATGCTTCTGTGTGCTAGCCAGGAAGCCCTTCGGTGGGG
CCCGCGGCTTTGAGGATGCAACCGGTTCTGGACGATGGCTGATCTCTGAATGATGTGTGGC
GGGGGCTGCTTTCGCTGGATTTCGCCGGTGTGGTTTCTGTGTGCTCTCTGCTGTGCTATCTCTG
CCCTGATCATGTCTGCTGCACCCCCAAAGGTGACGAGGACAGCTGCACATGCCCAAGGGGCCAAGAC
CCCCAGGGGAAGAGGGGTACACCGGCTCTCTCAGGAGTGGGAGGAGCAGCCGCAATCATCTGTA
GACGCTTGAAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGCAGAGCTTCAAG
TGGGACATGACCAAGCCAGCGATGCTGTGGCTGGGTCTGCAGACAGGCCCCCGCAGCAATCAG
GCGCACTCTGGGCTTCTGTCGATTCGAGCTGTCAGCAGGCGAGGTGACAGTGAAGTGAAGCTG
CCCAAGGATGTCAGCAGAGTGGCTTTCGATAGCTTCTGAGCAAGCGGGATGACTTGTGGAAACCTATT
CCTTAGCCGCCACCCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG
GATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG
CGATCATATAGAAGGATTTACCAAGACAAGAAAGGACAAGGAGCATTTGATAGCATCTACCTTCAA
AGATCAACAACAACAATCAAAACGCTCATTTTTCGACATTGACCGCATCATGAAGTGT
AAAAATGAAAGAACTCAACATGGCCCAACGCTTATCAATGTATTCTGCTCTAGCAAAAGGGTGG
ACAAGTTCCGGCATTTCAATGCAATTTTCAGGGAGATGTGCATTGACGAGGATGGAGAGAGCTCAT
CATGTTGTGTTTACTTTGGGAAGAAGAAATAATTAAGTCAAAAGAAATACTTTAAAAACATCTCAA
GCTGCCAATCTCAGGAATTTTACTTCTATCCAGCTGAATGGAAGATTTCTCGGGAAGAGGACATT
ATGTTGGAGCCCGCTTGTGGAAGGGAAGCAACCTCTCTTCTTTCTGTGATGTGCACATCTACTT
CATATCTGAATTTCTCAATACGTGTAGGCTGAATCAACAGCCAGGGAAGAAGTATTTTATCACT
CTTTTCAGTCAGTACAATCTGGCATATAATATACGGCCACCATGATGCTGCATGCTGCTGCTGCT
CTTTCTCTATAAGAAAGAAACTGGATTTTGGAGAGCATTTGAGTGGGCTGGCTGCTGCTGCTGCT
CTCAGACTTCAATCAATATAGTGTGGGTGCTGCTGTCGATCTGACATGACAGTCTGCTGCTGCTGCT
CTTTATCGCAAGTATCTCCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CTTCGATCGAGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CTTCGACAGTGAAGTCTCCACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CTTCGACAGCAACAACAAGACAAGATAGCAAAAAACAAGTCAATCCAGAGAAGAACTTCTGGGAGA
CACTTTTCTTCTTCTTCTGCAATTTCTGAAGTGGCTGCACAGAGAAGAACTTCCATAAAGGAC
ACAAAAGATTTGAGCTGATGGGTGAGATGAGAAGAACTCCGATTTCTCTCTGTGGGCTTTTATC
AACAGAAATCAAAATCTCCGCTTTGCTTCCAAAGTAAACCGAGTTGCACCTGTGAAGTGTCTGAC
AAGGCAGAAATGCTGTGAGATTTAAGGCTAATGTGTGGAGTTTGTATGTGTTTACAATACAT
GAGCGCTGTGTTTGTGTGCTCATGAATTTATCATGATTTAAGCAGTTTGTGAATAAATTCAT
TAGCATGAAGGCAAGCATATTTCTCTCATATGATAGCGCTATCAGCAGGGCTTAGTTTCTTAGG
AATGCTCAAAATATCAGAAGCGAGGAGGAGATAGGCTTATTATGATACTAGTGAATACATGAT
AAATAAATGAGCCACAAGAAAGAAAGAAACATAAATATGCTGCTCATATTTCTGCTTATGAT
AAATAAATCTCCTTATCTTTTGGTTGCTCTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GCACTTTTTCTGCTTGGAGTTATAGTGTGCTTATGATGATGATGATGATGATGATGATGATGATGAT
GCACAAAGTGGCTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GTCTCAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GAGTATTTTCGAAGGAGCACTCAACATGAGCAGTGGAGGAAAGAAATGACACTTCTGCTTACGGA
AAGGAACTCTCTCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GAAGTAGGGCCGCTCTTTACCTGTTTAAATAAACCAAGATACCGTGTGAACCAACAATCTCT
TTTCAAAACAGGGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
ATATATATATGCTGGAAGATCAATCAATCTGCAGAGATCTAGTGGGATGGAAGTGTCTTGTGCTAC
GTTATTCACCCAGGCGGAGTGAAGATCAATGAAATTTTTTAAATAAGAGCTTCTACTCAATCA
CCAAGATGCTCTGAAATGTGATTTTATACCATTTCAAACTCTTTTAAATAAATAACAGTTA
ACATAGAGTGGTTTCTTTCATCTGTAATTTAGCAATTTATGCGACGACCATGATGACAGTGAAT
CTTTGAGCTTTGCTTCTGTTGCTCAGATTAACCTCATGTTTAAAGCCCTGCTGCTGCTGCTGCTGCT
TGTGGTGTGTTAAAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AGGCCATGAATGGAAGTGGTATTCGACAGCTAATAAATATGATTTGTGGATGAA

FIGURE 276

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMAANTLINVIPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDLTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

099044-1150

FIGURE 277

GAAAGAA**ATGT**TTGTGGCTGCTCTTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGACAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAAATTGAAAATGGCATCCCCTCTGATCCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCAT**GAC**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCTGCTTCTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGAATAAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACGAC
 TCAAAATATTTCTAAAATATTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCATTTTGTGACCATTTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

0990441.1.F661

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

FIGURE 279

AACCTCAAACCTCCTCTCTCTGGGAAACACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAATATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAGGACGGGTGTCTTGGGATGGGAATCTGAGCGGTAGCA
TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACTGCCAGGTGA
AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTAGAAGACACAGACT**TAACA**ATTTTAGATGGAAGCTGAGATGATTTCCAAGACAA
GAACCTAGTATTTCTTGAAGTTAATGGAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACAGTTCTGACGATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
GTGTAATATTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCTTAA
GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGACATAAAAGCC
AATTTGTCTGTTACATTTCCCTTTCACGTATTTCTTTAGCAGCACTCTGGCTACTAAAGTTA
ATGTTGTTACTCTCTTCTCTCCCACTTCTCAATTAAGGTGTAGCTAAGCCTCCTCGGTG
TTCTTGATTAAAGTAATCTAAATTCAAACTGTTAAAGTACATTTTATTTTTATGTCTC
TCCTTAACATAGACACATCTTGTTTTACTGAATTTCTTCAATATTCAGGTGATAGATT
TTTGTCG

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTGGGAGTTCCATCTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTTT
ATCCAAC TACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

109111-1110660

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**AATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTCAAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTGTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGCTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCGTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTGTGTCCAGT**TAA**AACACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTGTCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTA**AA**ACTGAGAAAT
GGGCGGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCCAGCTGGCCCAACATGGTGGA**AA**ACTTGTCTACTATAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCTAGCTAGTCCAGTACTCGGGAGGCTGAG
CGAGGAAATCGCTTAACCCAGGAGGCGCAGCTTGCAGTGAGCCGAGATCGCGCGGCTGAT
TCCAGCCTGGGCGCAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

0990044.11601

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
 GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
 CGGGGCCGGGATGCAGCCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGCGCTCCCAGCCTGAATCTGCCTGGATGGAAGTGA
 GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGTGAGGGAAGGACATGTA
 CCCTTTTCATGCCTACACACCCCTCATTTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRITIELLGQEVSRGRDAAQELRASLLETQMEEDIILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQLRLHTAALPA

0990044.11501

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAGGCCAGGA
 AGCACAGCAAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAAGTCAATGCCTTGAAGGAAATCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACGTGTCTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGAGCAGCAAGAGATACATATGCGAGTTACCATCCC
 TAAATAGGCTCTTTCTCCAATGTGTCTCCAAGCAAGATTCAATCAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGTCTAACACATTTCTTTGGGATTTTGGCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTTCAGCCCATTACCCTTATTTTGAATTGCTCCATCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAAACGAATTTAAAGAATGCTATCTTGAAAAATTGCATACGCTGTGTCAATT
 TTTTATCTGCTAGTGTCTATTCTGCTTGTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTGAAGCAACAATTTT
 AAATATATTTTGTTCCTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACAATAT
 CCCACTTTGCAAACCTTTAACTACACATGCTTGGAATTAAGTTTGTAGCTGTTTCATTGCTCA
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVLGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLS
SLGIPVNHLEGSQKCVaelGFPQAVGAVKALKALLGALTVFG

090244 11504
109111 110200

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTACGCCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCGCCAACCTGGAAC
 GGGCCTCTCACAGGGGAGTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAAGAGACTCGGGGGAAAATTCCCAAAC
 GTTTGATGAGATTAATCTGAAACCAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTAC
 AAGACCATTAAAGGTGCCCATGATGTACGGTGCAGGCAAGTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTGTCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCAAGACTTGGTGGAGACA
 TGGCTCAGAACATGAAAACCCAGAAACATGGAAGTTTTCTTCCGAAGTTCAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCCACCCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACGTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCATGCTCTCTGTGTCATCAAAGTGGACCGGCCATTTTCATTTATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTCTGAACCTTATATATATTTTCTTACATACATACCTATGAT
 AAAGTTTAAATTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACATCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAAATTA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAAATGGCATTGC
 TGCTTAAAGCTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTTGGACCATTG
 TGACCATGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAATTTGATACATATTTTTTAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGAGAGAAGGACACACAGCTGTGGTGGTGTGTTCCC
TGTCAGAAAGCCGAAACTCTTTGACCACCGAGGAGAAGCCACAGAGTCAAGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCAGGACACCTGGGCCGTGTCTGTAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCGAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCCGTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAATAAACCCCGCAGGCAGCA
AAAAA

FIGURE 294

MRLLLLVTSLVVLLWEAGAVPAKVP IKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGFILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

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AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAAGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTG
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGTGGACCCCTGGTGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGCGGCCACGAGCG
ATGAGTACAAGAACCTTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCACGCGGAT
TGTTCAGTTTCAAGGATATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTTCTGCTTTTGTGATGGAGTGGAATGAAGCACTCATGTTGGTTA
CAGCAGACGCCGTGAGATAAATCAGGCAGCTGTGCTTCTATTCTATCGTTGACAGTTTTGTG
GGAGGGAACCCAGACCTCTCCTCCCACCATGAGATCCCAAGGATGGAGAACCACTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCTTGCCTCGGAACAATGGGACTCGGCGCGGAGGTGCTTGGGCCG
 CGCTGCTCTTGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAATGTATTACTCAAGAAAGGCATTTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATTCT
 CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGGCGACCCTGTGGGGAGGC
 CTTCCTTCGGCTTGCTCCTTGCTCAGCCTGTCTGCTGGCGCTTTCCTGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAATTCGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATCTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAAGTGTGTAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCTCAGCTAATGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAAGTCTGCTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAAAGTGAAGCAAAAGTCTGCTTGATTTTTTTTTCTTGTTTAAAGTA
 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATATCTTGAAGTCTTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTGTGTTGTTTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTTCAAGTCACCTTTACTAAACAAACTTTTGTAATAGACCTTACCTTCTATT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACCTGACTGTATTATCTGGGTATCTGCTGTGCTGCACCTTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAAGTGGCCATTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTTGCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGGCTTTT
 TCTTCTATGTCCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCA

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FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSVTIKVTIIYYLSILG
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYA
QQRWKLQVQEQ
RKSVFDRHVVLS

009044.11601

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGCTCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGA AAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

MAYSTVQRVALASGLVLLALLLPKAFLSRGKRQEPPTPEGKLGRRFPMMHHHQAPSDGQT
 PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFGLFYILYILFKVSRILIL
 ILHQ

1994-1995

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCAGTGTTCGCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGCAAATGTATATCAAGAT
AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGTATACTATTACATCCA
ATCTCAGTGTGCCTATTGGGCGCTCCAGAACCCGCTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGTGTCATGTGGTGGATTGATTGAGTGGGATGTGTTTCCAG
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAAGGA
GGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCGAGCACTGGG
GCCACTTCCGAATCTGTGTGAACCTGGTGGGGACATTTTCGCAATGACGGGTCCCATCATG
CTTCAAGGAGTGGGAGTGCAGATGGAGGAACTACACTGCAGTATCCACCTAGGGAACCT
GGTGTTCAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACC
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTAAAAATCAGAGGCCACTTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAAGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTCAGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCTGTGTGTCTCTGGGCCACTCTACCAGTGATTTGAGACTCCCGCTCTC
CCAGCTGTCTCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
TCTTGAGTGGGACACTTGGCCCTGGGAACCAAGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCCCTCTGTGGCGAGGGTTCTTAGTGAGTAGTTACTTGGGAAGCAATCAGAGATA
AAAACCAAGCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYNSLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLRMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWP SLR
SDRNN SLEKKS GGGMPKTQQAF

090044.11501

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAATGCAGCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAACATATTATTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMAILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARHLIRWVGLSRQKSNEVVKWEDGSVISENMFEL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

0990044.11601

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCGCTCCGCTGCCAGTCTCGCCCGGATCCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
 GCCCCGGCAAAACGAGGCTAAGGAGACCAAAGCGCGGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCGAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG
 CAGAGTTCATACTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVFSRVKLFSGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKLFKESVVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

3080441-1166

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTTGGCAGGAGTGTGCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAAGTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCGAG
 CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCG
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTGT
 CTGTCCAAGTGCGACTGTGCGGGGGGCGGCCGCGCGGCGCGGACC GCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAAGTCCCTTACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTGCGCGCATTTACAGCTGAGTGTGCGCTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGGCCTCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCACTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIHQKREVREPGGSRPVSQRRVCPRGTKSLCQKQLLLLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLAQNPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

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FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGC GCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTATATATGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSPASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGI VTRLYCRRQGYLLQMHPDGDALDGTGKDDSTNSTL FNLIPVGLRVVAIQVTKGLY
IAMNGEGYLYPSELFTPECKFKESVFENYGVYSSMLYRQGESGRAWFLGLNKEGQAMKNGR
VKTKPAAHFLPKPLEVAMYREPSLHDVGVETVPKPGVTPSKSTSASAIMNGGKPKVNKSKTT
```

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

GGGGAGGAGGAATTGACCATGTAAGAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTCCCTTGCAAAAAA
GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAATGATTGTGCAGAGAGAAGGAAGA
ACGAAGCTTTTTCTTTGTGAGCCCTGGATCTTAACACAATATGTATATGTGCACACAGGGAGCAATCAAGAAT
AAATAAACACGAGTTAGACCCCGGGGGTGGTGGTGGTCTGCATACATAAATAAATCTTTAAAGCAGCTGTCC
CTCCCAACCCCCAAAAGAGATGATTGAAATAGAGAACCGAGGATGACAAAGAAAAGTAATGTCTTATT
TTCTCTATAAAGGAGAAAGTGAGCCAGGAGATATTTTTGGAATGAAAAGTTTGGGSCTTTTTAGTAAAGTAA
AGAACTGGTGTGGTGGTGTCTTTCCCTTTCTTTTGAATTTCCACAAGAGAGAGGAAATTAATAATACATCTGC
AAGAAATTTAGAGAGAAGAAAGTGACCGCGGACGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
CAGTTGGATTTTGTGCCTATGTTGACATAAAATGACGGATAATTCGAGTTGGATTTTCTTCATCAACCTCTCT
TTTTTAAATTTTATTTCTTTCTTTGGTATCAAGATCATGCGTTTTCTCTTTCTTAAACCATGGATTTCCATCT
GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAGAGGACCAACACCAGATAAATATGATG
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGTTTAAACAGGGCCCTTTGACCCCT
GCTTGGTGGTGTCTGTGGCTCTTCAACTCTTGTGGTGGTGGTCTGTGGTGGGCTCAGACCTGCCCTCTGTGT
GCTCCTGCAGCAACCGATTCCGACAGGTTGTTGTTCGGAACCACTCGCTGAGGTTCCGGATGGCATCTCC
ACCAACACACGCTGCTGAACCTCTCAGAACCAATCCAGATCATCAAGTAGAACAGCTTCAAGCATCTGAG
CGATCTGGAATCTCTACAGTTGAGTAGGAACCATACAGAACCATTTGAAATTTGGGCTTTCAATGTTCTGGCGA
ACCTCAACACTCTGGAACCTTTGACATCTGCTTACTACCATCCCGAATGGAGCTTTTGATATCTGTCTAAA
CTGAAGGAGCTCTGGTTGCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAAATCCTTCTT
TGGCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGAAGTGCCCTTTGAAGAGTTGTCCAAT
CGGCTATTTTGAACCTTGCATGATTCAGGCTTCGGGAAATCCCTAACCTACACGCTCATTAACATAGATGAG
CTGGATTTTCTGGCAATCATTATCTGCCATCAGGCCTGGCTCTTTCCAGGTTTGATGCACCTTCAAAAAT
GTGGATGATACAGTCCAGATTCAAGTGATTGAACCGAATGCCTTTGACACCTCTCAGTCTAGTGGAGATCAT
ACCTTGGCACAATAATCTTAACTTACTGCTCATGACCTCTTCTACTCCCTTGATCATCTAGAGCGGATACAT
TATACATCACAAACCTTTGGAAGTGTAACCTGTGACATCTGTGGCTGAGTGGTGATGAGAGACATGCGCCCTC
GGACACAGCTGTGTTGCCCGGTGTAACCTCTCCAACTTAAGGGGAGGTGATCTGGAGAGCTCGACCAGA
ATTACTTCACTGTATGCTCCCGGTGTAATTTGTGGAGCCCTCGACACCTCAATGTCACTGAAGGCATGGCAGCT
GAGCTGAAATGTGCGGCTCCATCCCTGACATCTGTATCTTGGATTACTCAAAATGGAACAGTCTAGACACA
TGGGGCGTACAAAGTCGGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCACAAAATGTAACGTGCAGAGTA
CAGGCATGTACACATGTATGTTGAGTAATCTCGTTTGGGAATCTACTGCTTCCAGCCACCTGAATGTACTGCA
GCACCACTACTCTCTTTCTTACTTTTCAACCGTCAGATAGACATTTGAAACCGCTCAGGATGAGGCACG
GACCACAGATAACAATGTGGTCCCCTCCAGTGGTGCAGTGGGAGACCACCAATGTGACACCTCTCTCACAC
CACAGAGCACAAGGTGCAGAGAAAACTTCAACATCCAGTGACTGATATAACAGTGGGATCCAGGAAT
GTGAGGTCATGAAGACTACCAAAATCATCATTTGGTGTTTTGTGGCCATCAGCATCTGAGTGCAGTGTCT
GGTCACTTTTCAAGATGAGGAAGCAGCACCTCGGCAAAACCATCACGCCCAACAGGAGCTTTGAAATTA
TTAATGTGGATGATGAGATTACGGGAGACACCACTTGAAGGCCACTGCCATGCCTGCTATCGAGCTGAG
CACCTAAATCACTATCTACAAATCTCCCTTCAACCACACAACACAGTTAACACAATAAATCAATACA
CAGTTCAGTGCATGAACGTTATTGATCCGAATGAATCTTAAGACAAATGTACAAGAGACTCAAAATCAAACAA
TTTACAGAGTTACAAAAAACAAATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTAA
ATCTACTGTTTCAAAAAGTGCTTTACAAAAAAGAAAAAGAAATTTATTTATTAATAATCTTATTTG
TGATCTAAAGCAGCAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGIISTNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
 YISEGAFEGLSNLRYNLNLAMCNLREIPNLTPLIKLELDLDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGMYTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGTPVVDWETTNVTTSLTPQ
 STRSTEKTFTIPVTDINSIGPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

GC GCGCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGGCGGCTCCGCCCGGCACAT
GGCTGCAGCGCACTCGCGGACACCCGAGCGCGCGCCAGCTCGCCCGAGGTCGTCGGGA
GGCGCCGGCGCCGCCGGAGCAAGCAGCAACTGACGGGGGAAGCGCCGCGTCGGGGATC
GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCTCATATATGTGGAACCTTGGGGATCA
CACTGAGATCAAGAGATGGCGAGGAAAAGGCTCTTGCCCTGCCACCTCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATGTAATGGCTGCTCACCGATAATGAAGGAAACAAAA
GTGGTGATCACTTACTCCAGTCGTCTATCTACAAACTGACTGAGGAACAGAAAGGCCG
AGTGGCCTTTGCTTCCAATTTCTGCGAGGAGATGCTCTTGCAGATTGAACCTTGAAGC
CCAGTGATGAGGGCCGGTACACTGTAAGGTAAAGAATTCAGGGCGCTACGTGTGGAGCCAT
GTCTATCTTAAAGTCTTATGAGACATCCAGGCCAAGTGTAGTTTGAAGAGGAGCTGAC
AGAAGGAAGTGAAGTGAAGTGTGAGTCACTCTCGGCAGAGGCCATCTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAAGGGAGAGATGAAGCTCTGCCCTCCAAATCTAGGATT
GACTACAACCCAGCTGGACGAGTCTTGCTGCAGAAATCTACCATCTCTGACTGTGA
CCAGTGCACAGCGAGGCAAGAGCTGGGGAAGAAAGCTGTGTGGTGGCAGTAACGTGACAGT
ATGTACAAGAATCCGCGATGGTTGCGAGGACAGTGCAGGCGATAGTGCTGGAGCGCTGCTG
ATTTTCTCTTGTGTGGTCTGCTAATCCGAAGAAAGACAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTGTGTAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCTCCATCGCTCCAGCAAAAT
AGTGCTCTCAGCGACGCGGACACTGTCAACTACGCGACCAACCCAGCGAGGCTGGCCAC
CCAGGCATACAGCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACATCT
CTAATCTGACCAAAAGCAAAACCCAGCCAGATGATCCCCAGCCAGAGCAGGCTCTCCAA
ACGGTCTGAATATAACATGGACTGTGACTCCACGCTTTCCTAGAGATCAGGGTCTTTGGACTC
TTCTGCTCATTGGAGCTCAAGTCAACAGCCACACACAGATGAGAGGTCACTTAAGTAGCA
GTGAGCTTAACCGGAAACAGATTTCAGATGAGCATTTTCTTATACATCAAAACAGCAAA
AGGATGTAAAGCTGATTCTGTGTAAGGAGCATCTTATTGTGCTTTAGACAGGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTTGTAGCAAGGACCTGTGGTGAGAAGTTGGGGAAGGTG
AGGTGAATATACCTAAAATTTTAATGGGATATTTGATCAGTGGCTTGATTCACAAT
TTCAAGAGGAAATGGGATGCTGTTGTAAATTTCTATGCATTTCTGCAAAATTTATGGATT
ATTAGTTATTACAGAGTCAAGCAGAACCCAGCGCTTATTACCTGTCTACACATGTAT
TGAGTCTAACCACTCTAAGAAATCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TGATTTGTCTAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGTAGGAA
AGGATGAATGAGTTTCTCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAC
TATGAAAGGAGACAAAAATTTGTGAAACAGGATTTGTGAAGAGTTTCCATCTCTATGATGTT
ATGAGGATTTGTGACAAACATTAGAAATATATATGTGGAGCAATTGTGGATTTCCTCTCAAT
CAGATGCCCTCAAGGACTTCTGCTAGATATTTCTGGAAGGAGAAATACAACTGTCTATT
TATCAACGTCTCTTAGAAGAAATTTCTTAGAAGAAAAGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATTTATAGTCTCTTCTTGTAGAAAATGTGAACCAAGAAATGCAAGACTGG
GTGGACTAGAAAGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTTAGGAAATAATCCAGCGAGGTGGAGTGCAGTGAGCCGAGATTATGCC
ATTGCACTCAGCCTGGGTGACAGAGCGGGAATCCGCTCTC

FIGURE 316

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
```

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETGSDLTLCCESSGTEPIVYVQRIEREKEGEDERLPPKSRID
YNHPGRVLLQNLTSYSGLYPCTAGNEAGKESCVRVTVYVQVSGIMVAGAVTGIVAGALL
FLRWLLTIRRKDKERYEEEREPNEIDEAPKARLVKPSYSSGSRSSRSGSSSTRSTANS
ASRSORTSLTDAAPQGLTAQYSLVGEPRVSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACAGGAGCGAGAGCCGCCTACCTGCAGCCGCCGCCACGGCAGGGCAGCCCA
 CCTAGCGCGCTCCTGCTGTGCTCTCGTCTCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGGATATCACTACT
 CCTGAAGACATGTTGAAAAAAGCCAAAGGGGAAACTGCCCTATCTGCCATGCCAAATTACGCTTTAGTCCCGAACA
 CCAGGGACCGCTGGACATCCAGTGGCTGATATCACCAGCTGATAATCAGAAGTGGATCAAGTGATTATTTTAT
 ATTTCTGGAGACAAAATTTATGATGACTACTATCCAGCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGATGCATCAATAAATGTACGAATTTACAACCTGTCAGATATTGGCACATATCAGTCCAAATGTTACG
 AAAAGCTCCTGGTGTGTCAAATTAAGAAGATTTCATCTGGTAGTTCTTTGTTAAAGCTTCAGGTCCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCRATTACAG
 TATGAGTGGCAAAAATTTGCTGACTCACAGAAAATGCCACCTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAAACAGAGTGGCTCTGATC
 AGTGCTGTGTGCTCTAAACGTTGTCCTCCTTCAAATAAAGCTGGACTAATTGCAGGAGCCATTATAGGAACCT
 TTGCTTGTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGCTGAAGGCGCAGAGAGAAAAATATGAAAA
 GGAAGTTTCATCAGATATCAGGGAAGATGTGCCACCTCCAAGAGCCGTCAGTCCACTGCCAGAGCTACATCG
 GCAGTAATCATTATCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATCCAAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCCTCAGAGTCCGACTCTCCCACTGCTAAGTTCAGTACCCCTACAA
 GACTGATGGAATTACAGTTGTAATAATATGGACTACTGAAGAATCTGAAGTATTGTATTATTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTTAAATGTTTAAAAAAGCACAGGCGACAGAGATTAGAGCAGCTGAAGAACAC
 ATCTACTTTATGCAATGGCAATTAGACATGTAAGTCAGATGTCATGTCAAAATTAGTACGAGCCAAATTCCTTGT
 TAAAAACCTATGTATAGTGAACATGATAGTTAAAGATGTTTATTTATATTTTCAATACTTACCCTAACAA
 ATTTTAACTTTTCATATGCATATTCGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTCAA
 AGGAAATTTTAAATTTCTACGTTCTGTTAATGTTTGTCTATTAGTAAATACATGGAAGGGAATACCGG
 TTCTTTTCCCTTTTATGCACACAACAGAAACAGCGGTTGTCATGCCTCAAATATTTTATTTGCAACTACA
 TGATTTCAACAAATCTCTGTAACACAGACATAAAATAGATTCTGTATATAAATACTTACATACGCTCCA
 TAAAGTAACTTTCAAAGGTGCTAGAACAAATCGTCCAGTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATATTAATACTTAGGCACCTGACTAATCTTAATAAAATTTCTCAAACATA
 TATCAATATCTAAAGTGCATATATTTTAAAGAAAGATTATCTCAATAACTTCTATAAAAAATAAGTTTGATGG
 TTTGGCCCATCTAATCTCCTACTATTTAGTAAAGACTTTTAACTTTTAAATGTGTAGTAAAGGTTTATCTACCTT
 TTTCTCAAGATGACACCAACACCAATCAAAAACGAAGTGTAGTGAGGTGCTAAGATGTGAGGATTAAATCCAGTGAT
 TCCGGTCACATGCAATTCAGGAGGAGGTACCCTATGCTCACTGGAATTTGGCGGATATGGTTTATTTTCTTCCC
 TGATTTGGATAACCAATGGAACAGGAGGAGTATGATCTGTATGCGCCATTCCCTCGATACATCTCTGGCTT
 TTTCTGGGCAAAAGGGTGCACATTTGAAGAGGTGGAATATAAGTTCTGAAATCTCTAGGGAAGAGAACAT
 TAAATTAATTCAAAGGAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACAACT
 GAGATCACATCTAAGTGAACCTCTATTGTCAAGTCTAAATACATTAACAACTCATGTATAGCGGTATAA
 TGTATAACAGGTGACCAATGTTTCTGAATGCATAAAGAAATGAATAACTCAACACAGTACTTCCCTAAACAA
 CTTCAACCAAAAAGACCAAAACATGGAAACGAATGGAAGCTTTGAAGGACATGCTTTGTTTACTCCAGTGGTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATCAAAAACATTTGAGCTGGAGCCATTATCCTT
 AGCAAACTAATGCAGAAACAGAAATCACTACCGCATTTCTCACTTAAATGGAGTATGATTAAGAAT
 TATGAACACAAGAGAGGAACATAGACATTTGGAGTCTATTGAGAGGAGGGGTGGGAGAGGAAAGAGCA
 GAAAGATTAATCTTTGAGTACTGCTTCCACCTGGGTGATGAATAATATGTACACAAATCCCTGTGTACACA
 GTTTTACCTATGGAACAAACCTTCATGTGTATCCCTAAACCTAAATAAAGTTAAAAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

09900447.11.15.01

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCGCTGTGATGGTGA
 ATGGTGAAAGTGCGCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGTCTGGCGACAGCCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTCTACTTGAAAACCTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCACAACT
 TTGTTCTCATCGTGTACAACCTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTCTGCTATTCGGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAGGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTGTGTTCCCTGTGTCATTTCA
 AACAGTCTCCCTTCCATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACCTCAGAGCATGAAAAACACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGTGGGGTAAGGTGCATCTGTTTGAAG
 TAAACGATAAAATGTGGATTAAAGTCCCAGCACAAAGCAGATCCTCAATAAACATTTCAIT
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMCMVVLPCLGFTLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRREFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFKYL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

320/330

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACACGGTCTCAGGAGATGTCGTATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCCAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTACCTATGA

FIGURE 322

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLGLTILILCSVDNHGLRRLCLISTDMHHIEESFQEIKRAIQAKDTFPNVVTILST
 LETLQIKPLDVCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
 ROCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

amino acids 1-18

amino acids 56-60, 135-139

amino acids 102-106

amino acids 24-30

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACCGGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGGCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGCAGTGTGGGGCCCCGCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATGCCA
ATGCTCTCCCACTGTCTCGGCTCCAGTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTGGATCACACTATTTTCGAC
CCGGAGAAGTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
TCAGTATCACTTCTGTGTGCTGTGGGCCGGGCGAAGAGAGCCTTCTTCCAGGCATGAACC
CACCCCGTACTCCCAGTTCTCTGTCCCGGAGGAACGAGATCCCCCTAATTCATCTCAACACC
CCCATAACACGGCGGCACACCCGGAGCCGGAGGACGACTCGGAGCGGGACCCCTGAACGT
CTGAAGCCCCGGGCGCGGATGACCCGGCCCGGCTCTGTTCAGAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCATGGCCAGTGACCATTTAGGGGTGGTCAGGGGCGGTGAGTGAAAC
ACGACGCTGGGGGAACGGGCCCGAAGGCTGCCGCCCTTCGCCAAGTTTCATCTAGGGTGC
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAACCTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGACACCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCAACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCTCTGCTGAAGCCTTGGTGACTGTCACAAACCTCGAG
GTTATTAATTGCAGCATCAGAAATAGAACAACAACCTTCAGCATCTCTTGGGCGCTCAGA
CATAGATCTCATGCCCCAGGAAGGGGTGAAGGCCTCGTCCACTCCGATCCACCAGCTCTGC
CTGACTCTCACTGAAGCAAAACCACATCACTGAGGTACACAGCCTCTGCCGAGACCTGTCC
ACAGCCGGCACCCAGAGTCACTGCACTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTACGAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCTCTCTACAGCCCTCGGAAGCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCCCT
CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGACCTTAGCCAA
GATCACAACTCAGCGAAGACCAGATGAAGCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGACCT**TGA**GTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCACAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTGAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTTAGCCTG
GGCCCCACCAGCAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCTCGCTCATACCTCAC
CGAGTGATGATGATGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGACTACCTTGG
CATAGTCTTGTGTTTCAGTAAGAGAGACCTGATCACCATCTGTGTGCTTCCATCCTGCA
TTAAATTCACCTCAGTGTGGCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHALETQTL
ETSSRASTPAGPIPEAETRGAKRISPARETRSFKTSPNFMVLIASTVETSAASGSPEGAGM
TTVQITITGSDPEEAI FDTLCTDSDSEEAKLTMDILTLAHTSTEAKGLSSESSASSDGPHV
ITPSRAESSASSDGPHVITPSRAESSASSDGPHVITPSWSPGSDVTLAEALVTVTNI
EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPSTRD
PLPSVPPTTNTSSRGNTSLAKITTSAKTTMKPQQRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCCGCGCGGATTGCGCGGTCTTCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGCGACCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CTTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTGCTTCTCGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCATTGAAACACGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTTCTC
 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAACAGTACGGCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
 TATTTTGAAGACAGGAAAATGCCCTTCTGCTTTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGATCTCGGCTCTCACCAGAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTCAACATGTTGGTCAGGCTG
 GTCTCAAACCTGCTGACCTAGTGATCCACCTCCTCGGCTCCCAAAGTCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGTAATCTGTCTCTAAATATTAGCTAAAAACAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTATGCAAA
 GAAACAGGTTAGGACATAGGTTCCAATTCATTACATTCTGGTTCAGATAAAATCAAC
 TGTTTTATCAATTTCTAATGGATTGCTTTTTCTTTTATGGATTCTTTAAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVLIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQSFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVFLVIGLVLLGRILSES LRRKRYSRDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGACGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGAAGAAGGCGAGGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
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 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCTTGGGC
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 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGATGCT
 GGGGTGAGACTGGGATTTCTGGCTTCTTCTTGAACCACTGCATCCAGCCCTCAGGAAGCCT
 GTGAAAAACGTGATTCCTGGGCCCCACCAAGACCCACCAAAACCTCTCTGGGCTTGGTGCAG
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 ATGAACGCTCACACCCCTTCACTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
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0990447.1.11501

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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FFGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGGKTGAEEAPPLPG
TSQYGHERTSQYTGTSHPATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIPIVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128